

Wed Sep 10 08:50:53 2003

us-09-967-003-2.ra1

Page 1

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OW protein - protein search, using sw model

Run on: September 9, 2003, 23:29:38 ; Search time 15.375 Seconds
(without alignments)
8.256 Million cell updates/sec

Title: US-09-967-003-2

Perfect score: 15

Sequence: 1 RTR 3

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents, AA:*

- 1: /cgnt2_6/ptodata/1/1aa/5A.COMB.pep.*
- 2: /cgnt2_6/ptodata/1/1aa/5B.COMB.pep.*
- 3: /cgnt2_6/ptodata/1/1aa/6A.COMB.pep.*
- 4: /cgnt2_6/ptodata/1/1aa/6B.COMB.pep.*
- 5: /cgnt2_6/ptodata/1/1aa/PTUS.COMB.pep.*
- 6: /cgnt2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	15	100.0	3	4	US-09-521-365A-2
2	15	100.0	4	2	US-08-685-589A-61
3	15	100.0	4	2	US-08-685-589A-68
4	15	100.0	5	1	US-08-366-591-14
5	15	100.0	5	2	US-08-348-353-8
6	15	100.0	5	2	US-08-465-965-8
7	15	100.0	5	3	US-08-465-966-8
8	15	100.0	5	3	US-09-012-126-7
9	15	100.0	5	3	US-09-395-344-7
10	15	100.0	5	4	US-09-521-365A-3
11	15	100.0	5	4	US-09-546-483-6
12	15	100.0	5	4	US-09-823-177-6
13	15	100.0	6	1	US-08-264-002-11
14	15	100.0	6	1	US-08-064-111C-4
15	15	100.0	6	3	US-09-012-126-8
16	15	100.0	6	3	US-09-395-344-8
17	15	100.0	6	3	US-09-257-218-17
18	15	100.0	6	3	US-09-311-760-17
19	15	100.0	6	4	US-09-561-756-54
20	15	100.0	6	4	US-09-227-721-54
21	15	100.0	6	4	US-08-865-579-17
22	15	100.0	6	4	US-09-122-144-4
23	15	100.0	6	4	US-10-059-749-17
24	15	100.0	7	2	US-08-310-912A-90
25	15	100.0	7	3	US-08-841-089-90
26	15	100.0	7	3	US-09-301-085-90
27	15	100.0	7	5	PCT-US95-04570-90

28	15	100.0	7	5	PCT-US95-04589-90	Sequence 90, Appl
29	15	100.0	8	1	US-07-994-469A-15	Sequence 15, Appl
30	15	100.0	8	2	US-08-350-260A-376	Sequence 376, App
31	15	100.0	8	2	US-08-350-260A-449	Sequence 449, App
32	15	100.0	8	2	US-08-350-260A-456	Sequence 456, App
33	15	100.0	8	2	US-08-350-260A-459	Sequence 459, App
34	15	100.0	8	2	US-08-350-260A-508	Sequence 508, App
35	15	100.0	8	4	US-09-104-337A-376	Sequence 376, App
36	15	100.0	8	4	US-09-104-337A-449	Sequence 449, App
37	15	100.0	8	4	US-09-104-337A-456	Sequence 456, App
38	15	100.0	8	4	US-09-104-337A-459	Sequence 459, App
39	15	100.0	8	4	US-09-104-337A-508	Sequence 508, App
40	15	100.0	9	1	US-08-096-941-1	Sequence 1, Appl
41	15	100.0	9	1	US-08-464-318-5	Sequence 5, Appl
42	15	100.0	9	1	US-08-146-145-1	Sequence 1, Appl
43	15	100.0	9	2	US-08-700-035A-13	Sequence 13, Appl
44	15	100.0	9	2	US-08-471-341-5	Sequence 5, Appl
45	15	100.0	9	2	US-08-461-566-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-521-365A-2
Sequence 2, Application US/09521365A
Patent No. 6310041
GENERAL INFORMATION:
APPLICANT: Haddox, Jeffrey
APPLICANT: Pfeister, Robert
APPLICANT: Biaback, James
APPLICANT: Matteo, Villain
TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC USES TH
FILE REFERENCE: 92750/57
CURRENT APPLICATION NUMBER: US/09/521,365A
CURRENT FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: US 60/123,409
PRIOR FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 3
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: description of artificial sequence: amino acid
OTHER INFORMATION: sequence of complementary peptide inhibitor of
OTHER INFORMATION: neuropeptides; used as a monomer, dimer, and tetramer
US-09-521-365A-2
Query Match 100.0%; Score 15; DB 4; Length 3;
Best local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 RTR 3
1 RTR 3
1 RTR 3
1 RTR 3
RESULT 2
US-08-685-589A-61
Sequence 61, Application US/08685589A
Patent No. 5916872
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
NUMBER OF INVENTIONS: SPECTROM ANTIMICROBIAL ACTIVITY
CORRESPONDENCE ADDRESS:
ADDRESSER: Penne & Edmonds LLP
STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: No. 5916872 Relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..4
OTHER INFORMATION: /product= "Beta-turn"
US-08-685-589A-61

Query Match 100.0%; Score 15; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 RTR 3
111
1 RTR 3

RESULT 3
US-08-685-589A-68
Sequence 68, Application US/08685589A
Patent No. 5916872
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: No. 5916872 Relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..4
OTHER INFORMATION: /product= "Beta-turn"
US-08-685-589A-68

Query Match 100.0%; Score 15; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 RTR 3
111
2 RTR 4

RESULT 4
US-08-366-591-14
Sequence 14, Application US/08366591
Patent No. 5602021
GENERAL INFORMATION:
APPLICANT: Davis G., Claude
APPLICANT: Guay, Gordon G.
TITLE OF INVENTION: Method for Generating Proteolytic
TITLE OF INVENTION: Enzymes Specific Against a Selected Peptide Sequence
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,591
FILING DATE: 29-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 2222-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: CA2000-OMP2 tandem dibasic
INDIVIDUAL ISOLATE: recognition sites
US-08-366-591-14

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
|||
DB 2 RTR 4

RESULT 5
US-08-348-353-8
Sequence 8, Application US/08348353
Patent No. 5932217
GENERAL INFORMATION:
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,353
FILING DATE: 30-NOV-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, David
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-097CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-348-353-8

Query Match
Best Local Similarity 100.0%; Score 15; DB 2; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
|||
DB 2 RTR 4

RESULT 6
US-08-465-965-8
Sequence 8, Application US/08465965
Patent No. 5968512
GENERAL INFORMATION:
APPLICANT: Tuomanen, Elaine

APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,965
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/348,353
FILING DATE: 30-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,572
FILING DATE: 23-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03725
FILING DATE: 04-MAY-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/695,613
FILING DATE: 03-MAY-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, David
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-097CIP1DIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-965-8

Query Match
Best Local Similarity 100.0%; Score 15; DB 2; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
|||
DB 2 RTR 4

RESULT 7
US-08-465-966-8
Sequence 8, Application US/08465966
Patent No. 6015560
GENERAL INFORMATION:
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,966
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/348,353
FILING DATE: 30-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,572
FILING DATE: 23-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03725
FILING DATE: 04-MAY-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/695,613
FILING DATE: 03-MAY-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, David
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-097CIPDIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-966-8

Query Match 100.0%; Score 15; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
111
DB 2 RTR 4

RESULT 8
US-09-012-126-7
Sequence 7, Application US/09012126
Patent No. 6017735
GENERAL INFORMATION:
APPLICANT: O'Hare and Elliott
TITLE OF INVENTION: Materials and methods for intracellular transport and
FILE REFERENCE: 49408
CURRENT APPLICATION NUMBER: US/09/012,126
CURRENT FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-012-126-7

Query Match 100.0%; Score 15; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
111
DB 1 RTR 3

RESULT 9
US-09-395-344-7
Sequence 7, Application US/09395344
Patent No. 6251398
GENERAL INFORMATION:
APPLICANT: O'Hare and Elliott
TITLE OF INVENTION: Materials and methods for intracellular transport and
FILE REFERENCE: 49408
CURRENT APPLICATION NUMBER: US/09/395,344
CURRENT FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-395-344-7

Query Match 100.0%; Score 15; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
111
DB 1 RTR 3

RESULT 10
US-09-521-365A-3
Sequence 3, Application US/09521365A
Patent No. 6310041
GENERAL INFORMATION:
APPLICANT: Haddock, Jeffrey
APPLICANT: Plister, Robert
APPLICANT: Bialock, James
APPLICANT: Matteo, Villain
TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC USES THERE
FILE REFERENCE: 92750/57
CURRENT APPLICATION NUMBER: US/09/521,365A
CURRENT FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: US 60/123,409
PRIOR FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 5
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: description of artificial sequence: amino acid
OTHER INFORMATION: sequence of complementary peptide inhibitor of
OTHER INFORMATION: neutrophils; used as a monomer
US-09-521-365A-3

Query Match 100.0%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
DB 1 RTR 3

RESULT 11

US-09-546-483-6
; Sequence 6, Application US/09546483
; Patent No. 6358739
; GENERAL INFORMATION:
; APPLICANT: Baetge, Ed
; APPLICANT: Wong, Shou
; APPLICANT: Dupraz, Philippe
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: TRANSIENTLY IMMORTALIZED CELLS FOR USE IN GENE THERAPY
; FILE REFERENCE: 17811-011
; CURRENT APPLICATION NUMBER: US/09/546,483
; CURRENT FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/128,893
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Herpes simplex type 1 virus
US-09-546-483-6

Query Match

Best Local Similarity 100.0%; Score 15; DB 4; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
DB 1 RTR 3

RESULT 12

US-09-823-177-6
; Sequence 6, Application US/09823177
; Patent No. 6451601
; GENERAL INFORMATION:
; APPLICANT: Baetge, Ed
; APPLICANT: Wong, Shou
; APPLICANT: Dupraz, Philippe
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: TRANSIENTLY IMMORTALIZED CELLS FOR USE IN GENE THERAPY
; FILE REFERENCE: 17811-011
; CURRENT APPLICATION NUMBER: US/09/823,177
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 09/546,483
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/128,893
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Herpes simplex type 1 virus
US-09-823-177-6

Query Match

Best Local Similarity 100.0%; Score 15; DB 4; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
DB 1 RTR 3

RESULT 13
US-08-264-002-11

; Sequence 11, Application US/08264002
; Patent No. 5559019
; GENERAL INFORMATION:
; APPLICANT: GUI, JIAN-FANG
; APPLICANT: FU, XIANG-DONG
; TITLE OF INVENTION: NOVEL PROTEIN SERINE KINASE, SRPK1
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN TUBAS & LUBRITZ
; STREET: 1880 Century Park East, Fifth floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,002
FILING DATE: 22-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN PH.D., LISA A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD3590
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..6
US-08-264-002-11

Query Match 100.0%; Score 15; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
DB 2 RTR 4

RESULT 14

US-08-064-111C-4
; Sequence 4, Application US/08064111C
; Patent No. 5688760
; GENERAL INFORMATION:
; APPLICANT: Kemp, Bruce E.
; APPLICANT: Nicholson, Geoffrey C.
; APPLICANT: Martin, Thomas J.
; APPLICANT: Fenton, Anna J.
; APPLICANT: Hammonds, R. Glenn
; TITLE OF INVENTION: COMPOUNDS AND COMPOSITIONS WHICH INHIBIT
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,111C
FILING DATE: 12-AUG-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00580
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK9567
FILING DATE: 19-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK3879
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58456/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-064-111C-4

Query Match . 100.0%; Score 15; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
Db 1 RTR 3

RESULT 15
US-09-012-126-8
Sequence 8, Application US/09012126
Patent No. 6017735
GENERAL INFORMATION:
APPLICANT: O'Hare and Elliott
TITLE OF INVENTION: Materials and methods for intracellular transport and
FILE REFERENCE: 48408
CURRENT APPLICATION NUMBER: US/09/012,126
CURRENT FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-012-126-8

Query Match . 100.0%; Score 15; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
Db 1 RTR 3

Search completed: September 9, 2003, 23:36:07
Job time : 17.375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2003, 23:20:43 ; Search time 45 Seconds

(without alignments)
10.582 Million cell updates/sec

Title: US-09-967-003-2

Perfect score: 15

Sequence: 1 RTR 3

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	4	AAW52424	Beta-turn region u
2	15	100.0	4	AAW52417	Beta-turn region u
3	15	100.0	4	AAW52411	Antimicrobial cycl
4	15	100.0	4	AAW52404	Antimicrobial cycl
5	15	100.0	5	AAW52401	Streptokinase-bind
6	15	100.0	5	AAW52398	Streptokinase-bind
7	15	100.0	5	AAW52395	Peptide derived fr
8	15	100.0	5	AAW52392	Peptide inhibiting
9	15	100.0	5	AAW52389	Adenoviral NLS pep

10	15	100.0	5	21	AAW52418	Synthetic compleme
11	15	100.0	5	21	AAW52416	Transport activity
12	15	100.0	5	21	AAW52414	FHA peptide inhibi
13	15	100.0	5	23	AAW52411	Human immunoglobul
14	15	100.0	5	23	AAW52408	Glycoprotein cleav
15	15	100.0	6	16	AAW52405	Streptokinase-bind
16	15	100.0	6	16	AAW52402	Streptokinase-bind
17	15	100.0	6	17	AAW52399	NGP mucin epitope
18	15	100.0	6	19	AAW52396	Human microtubule
19	15	100.0	6	20	AAW52393	Conserved peptide
20	15	100.0	6	20	AAW52390	HIV-1 nucleic acid
21	15	100.0	6	21	AAW52387	Human secreted pep
22	15	100.0	6	22	AAW52384	Mammalian ced-3 ho
23	15	100.0	6	22	AAW52381	Human MCH6 conserv
24	15	100.0	6	23	AAW52378	Human caspase cons
25	15	100.0	6	23	AAW52375	Bacillus subtilis
26	15	100.0	6	23	AAW52372	Zinc finger recogn
27	15	100.0	6	23	AAW52369	RALV Env protein v
28	15	100.0	6	24	AAW52366	Human IgG Fc pepti
29	15	100.0	6	24	AAW52363	Herpes simplex vir
30	15	100.0	7	16	AAW52360	Streptokinase-bind
31	15	100.0	7	21	AAW52357	RTR dimer. Synthe
32	15	100.0	7	23	AAW52354	CXCR zinc-finger h
33	15	100.0	7	23	AAW52351	Human Blys binding
34	15	100.0	7	23	AAW52348	Transcription fact
35	15	100.0	8	20	AAW52345	Elastolytic peptid
36	15	100.0	8	20	AAW52342	Elastolytic peptid
37	15	100.0	8	21	AAW52339	RTR tetramer. Syn
38	15	100.0	8	21	AAW52336	Hyaluronate syntha
39	15	100.0	8	21	AAW52333	Human antibody fra
40	15	100.0	8	23	AAW52330	Human Fv molecule
41	15	100.0	8	23	AAW52327	ICK motif #6. Pla
42	15	100.0	8	23	AAW52324	Plant ICK protein
43	15	100.0	8	23	AAW52321	Plant ICK protein
44	15	100.0	8	23	AAW52318	Plant ICK protein
45	15	100.0	8	23	AAW52315	Plant ICK protein

ALIGNMENTS

RESULT 1
ID AAW52424 standard; peptide: 4 AA.
XX AAW52424:
AC
XX 01-JUL-1998 (first entry)
XX
XX Beta-turn region used in cyclic peptide of the invention.
DE
XX Beta-turn region; cyclic peptide; antimicrobial; disinfectant; therapy.
KW preservative; amphipathic anti-parallel beta-sheet region; plant disease.
KW
XX
OS Synthetic.
XX
XX
XX MO9803192-A1.
XX
XX 29-JAN-1998.
XX
XX 23-JUL-1997; 97MO-US12974.
XX
XX 24-JUL-1996; 96US-0685589.
XX
XX (INTR-) INTRABIOITICS PHARM INC.
XX
XX Chang C, Chen J, Gu L;
XX WPI; 1998-120472/11.
XX
XX New cyclic peptide(s) with antimicrobial activity - contain
XX amphipathic beta-sheet, loop and beta-turn regions, have better
XX activity, bioavailability and protease resistance than linear

PT analogues
XX
XX Claim 3; Page 149; 160pp; English.
XX
XX
CC This sequence represents a beta-turn region used in a peptide of the
CC invention. The peptides are cyclic peptides (I), which have: (a) in
CC amphipathic anti-parallel beta-sheet region (SR), a loop region (LR) and
CC a beta-turn region (TR); (b) a net positive charge at physiological pH;
CC and (c) at least one basic amino acid (aa) in LR or TR. (I) are broad
CC spectrum antimicrobials, specifically for use against *E. coli*,
CC *Pseudomonas aeruginosa*, methicillin-resistant *Staphylococcus aureus*
CC (MRSA), vancomycin-resistant *Enterococcus faecium* and
CC penicillin-resistant *Streptococcus pneumoniae*. More generally they are
CC active against Gram-positive or -negative bacteria, fungi, yeast and
CC protozoa. Apart from clinical uses, (I) are also used as disinfectants
CC and preservatives for medical equipment, foods, cosmetics etc., also for
CC treatment of plant diseases. Compared with non-cyclised analogues (I.e.
CC tachyplesin and protegrin type peptides), (I) and are more effective,
CC with better bioavailability and/or serum half-life (increased resistance
CC to proteolysis). They are more suitable for oral administration, can be
CC used at lower doses and are unlikely to induce development of resistant
CC strains.
XX
SQ Sequence 4 AA;
Query Match 100.0%; Score 15; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RTR 3
111
DB 2 RTR 4
RESULT 2
AAMS2417
ID AAMS2417 standard; peptide: 4 AA.
XX
XX AAMS2417;
AC
XX 01-JUL-1998 (first entry)
DT
XX
XX Beta-turn region used in cyclic peptide of the invention.
DE
XX
KM Beta-turn region; cyclic peptide; antimicrobial; disinfectant; therapy;
KM preservative; amphipathic anti-parallel beta-sheet region; plant disease.
XX
XX Synthetic.
OS
XX WO9803192-A1.
PN
XX 29-JAN-1998.
PD
XX
XX 23-JUL-1997; 97WO-US12974.
PF
XX
XX 24-JUL-1996; 96US-068589.
PR
XX
XX (INTR-) INTRABIOTICS PHARM INC.
PA
XX
XX Chang C, Chen J, Gu L;
PI
XX
XX WPI; 1998-120472/11.
DR
XX
XX New cyclic peptide(s) with antimicrobial activity - contain
PT amphipathic beta-sheet, loop and beta-turn regions, have better
PT activity, bioavailability and protease resistance than linear
PT analogues
XX
XX Claim 3; Page 149; 160pp; English.
PS
XX
XX This sequence represents a beta-turn region used in a peptide of the
CC invention. The peptides are cyclic peptides (I), which have: (a) an
CC amphipathic anti-parallel beta-sheet region (SR), a loop region (LR) and

CC a beta-turn region (TR); (b) a net positive charge at physiological pH;
CC and (c) at least one basic amino acid (aa) in LR or TR. (I) are broad
CC spectrum antimicrobials, specifically for use against *E. coli*,
CC *Pseudomonas aeruginosa*, methicillin-resistant *Staphylococcus aureus*
CC (MRSA), vancomycin-resistant *Enterococcus faecium* and
CC penicillin-resistant *Streptococcus pneumoniae*. More generally they are
CC active against Gram-positive or -negative bacteria, fungi, yeast and
CC protozoa. Apart from clinical uses, (I) are also used as disinfectants
CC and preservatives for medical equipment, foods, cosmetics etc., also for
CC treatment of plant diseases. Compared with non-cyclised analogues (I.e.
CC tachyplesin and protegrin type peptides), (I) and are more effective,
CC with better bioavailability and/or serum half-life (increased resistance
CC to proteolysis). They are more suitable for oral administration, can be
CC used at lower doses and are unlikely to induce development of resistant
CC strains.
XX
SQ Sequence 4 AA;
Query Match 100.0%; Score 15; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RTR 3
111
DB 1 RTR 3
RESULT 3
AA09621
ID AA09621 standard; peptide: 4 AA.
XX
XX AA09621;
AC
XX 21-JUL-1999 (first entry)
DT
XX
XX Antimicrobial cyclic peptide beta-turn region SEQ ID NO:68.
DE
XX
XX Cyclic peptide; antimicrobial; amphiphilic beta-sheet; bioactive;
KM biocidal; bacteria; yeast; candida species; fungi; protozoa;
KM *Escherichia coli*; *Pseudomonas aeruginosa*; infection; preservative;
KM vancomycin-resistant *Enterococcus faecium*; disinfectant; food;
KM methicillin-resistant *Staphylococcus aureus*; medical equipment;
KM penicillin-resistant *Streptococcus pneumoniae*; cosmetic.
XX
XX Synthetic.
OS
XX WO9921879-A1.
PN
XX
XX 06-MAY-1999.
PD
XX
XX 27-OCT-1997; 97WO-US19557.
PF
XX
XX 27-OCT-1997; 97WO-US19557.
PR
XX
XX (INTR-) INTRABIOTICS PHARM INC.
PA
XX
XX Chang C, Chen J, Gu L;
PI
XX
XX WPI; 1999-312941/26.
DR
XX
XX Antimicrobial cyclic peptides with amphiphilic beta-sheet region
PT
XX
XX Claim 3; Page 150; 167pp; English.
PS
XX
XX The present invention describes cyclic peptides (I): (1) comprising an
CC amphiphilic anti-parallel beta-sheet region (A), a loop region (B) and
CC a beta-turn (C); (II) having net positive charge at physiological pH;
CC and (III) including at least one basic amino acid (aa) in (B) or (C).
CC AA09554 to AA09683 and AA17301 to AA17385 represent specifically
CC claimed cyclic peptides and peptide segments. (I) are broad-spectrum
CC antimicrobials (biostatic or biocidal), effective against bacteria,
CC yeast (e.g. *Candida* species), fungi and protozoa. Particularly they
CC are used to control *Escherichia coli*, *Pseudomonas aeruginosa*,

CC vancomycin-resistant Enterococcus faecium, methicillin-resistant
 CC Streptococcus aureus and penicillin-resistant Streptococcus
 CC pneumoniae. (A) are used to treat or prevent infections in animals or
 CC plants, also as preservatives and disinfectants for medical equipment,
 CC foods, cosmetics, optionally as mixtures or in combination with other
 CC antimicrobials. Compared with linear analogues, (1) are more effective
 CC with better bioavailability and/or serum half-life (better resistance
 CC to proteolysis), allowing lower doses and making them more suitable for
 CC oral delivery). Since (1) are structurally related to naturally
 CC occurring antimicrobial peptides, they are less likely to induce
 CC development of resistant strains.

CC Sequence 4 AA:

Query Match 100.0%; Score 15; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 III
 DB 2 RTR 4

RESULT 4

AA09614 standard; Peptide: 4 AA.

AC AA09614;

DT 21-JUN-1999 (first entry)

DE Antimicrobial cyclic peptide beta-turn region SEQ ID NO:61.

CC Cyclic peptide; antimicrobial; amphiphilic beta-sheet; bioactive;
 CC bioactive; bacteria; yeast; Candida species; fungi; protozoa;
 CC Escherichia coli; Pseudomonas aeruginosa; infection; preservative;
 CC vancomycin-resistant Enterococcus faecium; disinfectant; food;
 CC methicillin-resistant Streptococcus aureus; medical equipment;
 CC penicillin-resistant Streptococcus pneumoniae; cosmetic.

OS Synthetic.

PN MO9921879-A1.

PD 06-MAY-1999.

PP 27-OCT-1997; 97WO-US19557.

PR 27-OCT-1997; 97WO-US19557.

PA (INTR-) INTRABIOLOGICS PHARM INC.

PI Chang C, Chen J, Gu L;

DR WPI; 1999-312941/26.

PT Antimicrobial cyclic peptides with amphiphilic beta-sheet region

PS Claim 3; Page 150; 167pp; English.

CC The present invention describes cyclic peptides (1): (1) comprising an
 CC amphiphilic anti-parallel beta-sheet region (A), a loop region (B) and
 CC a beta-turn (C); (1) having net positive charge at physiological pH;
 CC and (1) including at least one basic amino acid (aa) in (B) or (C).
 CC AA09554 to AA09683 and AA097301 to AA097385 represent specifically
 CC antimicrobial peptides and peptide segments. (1) are broad-spectrum
 CC antimicrobials (bacterial or bioactive) effective against bacteria,
 CC yeast (e.g. Candida species), fungi and protozoa. Particularly they
 CC are used to control Escherichia coli, Pseudomonas aeruginosa,
 CC vancomycin-resistant Enterococcus faecium, methicillin-resistant
 CC Streptococcus aureus and penicillin-resistant Streptococcus
 CC pneumoniae. (A) are used to treat or prevent infections in animals or
 CC plants, also as preservatives and disinfectants for medical equipment,

CC foods, cosmetics, optionally as mixtures or in combination with other
 CC antimicrobials. Compared with linear analogues, (1) are more effective
 CC with better bioavailability and/or serum half-life (better resistance
 CC to proteolysis), allowing lower doses and making them more suitable for
 CC oral delivery). Since (1) are structurally related to naturally
 CC occurring antimicrobial peptides, they are less likely to induce
 CC development of resistant strains.

CC Sequence 4 AA:

Query Match 100.0%; Score 15; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 III
 DB 1 RTR 3

RESULT 5

AA09675 standard; peptide: 5 AA.

AC AA09675;

DT 12-JAN-1996 (first entry)

DE Streptokinase-binding plasmin B chain peptide.

CC Streptokinase; plasmin B; affinity chromatography; purification;
 CC isolation.

OS Homo sapiens.

PN GR2284422-A.

PD 07-JUN-1995.

PP 29-NOV-1994; 94GB-0024112.

PR 29-NOV-1993; 93GB-0024473.

PA (OXFO-) OXFORD RES SUPPORT CO LTD.

PI Cederholm-Williams SA;

DR WPI; 1995-196178/26.

PT New peptide sequences from plasmin B chain - able to bind other
 CC proteins esp. streptokinase, useful for affinity purifcn.

PS Claim 3; Page 6; 14pp; English.

CC AAR75669-R75678 and AAR75682 are streptokinase binding peptides derived
 CC from the human plasmin B chain in the regions 576-600, 620-640 or
 CC 640-653 amino acids. The peptides are also capable of binding other
 CC proteins useful particularly when immobilised on a solid support for
 CC use in affinity chromatography.

CC Sequence 5 AA:

Query Match 100.0%; Score 15; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 III
 DB 1 RTR 3

RESULT 6

AA069572 standard; peptide: 5 AA.

```

XX AC AAM69572;
XX XX
XX DT 25-MAR-2003 (updated)
XX DT 07-DEC-1998 (first entry)
XX XX
XX DE Filamentous haemagglutinin antiinflammatory peptide III.
XX KM Factor X; filamentous haemagglutinin; FHA; endothelial cell;
XX KM integrin receptor; blood-brain barrier; antiinflammatory;
XX KM inflammation; meningitis; therapy.
XX OS
XX OS Bordetella pertussis.
XX OS Synthetic.
XX PN US5792457-A.
XX PD 11-AUG-1998.
XX PF 06-JUN-1995; 95US-0465929.
XX PR 30-NOV-1994; 94US-0348353.
XX PR 03-MAY-1991; 91US-0695613.
XX PR 04-MAY-1992; 92MO-US03725.
XX PR 23-MAY-1994; 94US-0247572.
XX PR 06-JUN-1995; 95US-0465929.
XX PA (UVRQ ) UNIV ROCKEFELLER.
XX PI Masure HR, Tuomanen E;
XX DR WPI, 1998-456074/39.
XX XX
XX PT Increasing blood-brain barrier permeability - with antibody to
XX PT filamentous haemagglutinin RGD regions
XX PS
XX PS Example 9; Column 32; 64pp; English.
XX XX
XX CC This peptide corresponds to amino acid residues 32-36 of
XX CC Bordetella pertussis filamentous haemagglutinin (FHA). Sequence
XX CC similarity has been found between amino acid residues 238-246,
XX CC 366-374 and 422-430 (see AAM69568-70) of Factor X and amino acid
XX CC residues 1979-1984, 2063-2068, 32-36 and 2528-2533 (see AAM69571-74)
XX CC of FHA. Inhibition of leukocyte-endothelial cell interactions by
XX CC these FHA peptides, which interact with CD11b/CD18 in the same
XX CC manner as Factor X, was demonstrated. The FHA peptides also
XX CC inhibit Factor Xa procoagulant activity on monocytes, and reduce
XX CC inflammation in an experimental (rabbit) meningitis model.
XX CC Protection against blood brain barrier permeability is also
XX CC afforded by the FHA peptides. FHA peptide III can be used in
XX CC quality control procedures to test for the presence of antigens
XX CC in vaccines which will generate toxin antibodies.
XX CC (Updated on 25-MAR-2003 to correct pf field.)
XX SQ Sequence 5 AA:

Query Match 100.0%; Score 15; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
   |||
   2 RTR 4
Db

RESULT 7
AAY43556
ID AAY43556 standard; peptide; 5 AA.
XX
XX AAY43556;
AC
XX
XX 26-JAN-2000 (first entry)
DT
XX

```

```

DE DE Peptide derived from a region of FHA with Factor X similarity.
XX XX
XX KM Filamentous haemagglutinin; FHA; Factor X; leukocyte;
XX KM blood vessel endothelial cell; migration; inflamed tissue;
XX KM non-fimbrial surface associated protein; Bordetella pertussis; C3b;
XX KM RGD tripeptide; integrin receptor; inflammation; antibiotic therapy;
XX KM infection; meningitis; septic arthritis; endophthalmitis;
XX KM autoimmune disease.
XX OS
XX OS Synthetic.
XX OS Bordetella pertussis.
XX PN US5968512-A.
XX PD 19-OCT-1999.
XX PF 06-JUN-1995; 95US-0465965.
XX PR 30-NOV-1994; 94US-0348353.
XX PR 04-MAY-1992; 92MO-US03725.
XX PR 03-MAY-1991; 91US-0695613.
XX PR 23-MAY-1994; 94US-0247572.
XX PA (UVRQ ) UNIV ROCKEFELLER.
XX PI Masure HR, Tuomanen E;
XX DR WPI, 1999-600812/51.
XX XX
XX PT Peptides inhibiting the influx of leukocytes into inflamed tissue,
XX PT useful for dampening the inflammation during treatment with antibiotics -
XX PS Claim 2; Column 75; 81pp; English.
XX XX
XX PS AAY43549-66 represent filamentous haemagglutinin (FHA) and Factor X
XX CC peptides which interact with leukocytes or with blood vessel endothelial
XX CC cells, thereby inhibiting the migration of leukocytes from the blood
XX CC steam into inflamed tissue. FHA is a non-fimbrial surface associated
XX CC protein secreted by Bordetella pertussis. As there are four regions in
XX CC FHA with sequence similarity to three regions in Factor X, some
XX CC antibodies to these four regions cross-react with Factor X, and vice
XX CC versa. The FHA peptides of the invention are derived from these regions.
XX CC FHA peptides competitively inhibit binding of Factor X and C3b1 to
XX CC leukocytes. Specifically, the peptides inhibit the reaction between the
XX CC RGD tripeptide of FHA and the integrin receptors of endothelial cells.
XX CC The FHA peptides (and antibodies to them) dampen inflammation during the
XX CC course of therapy with antibiotics and are therefore useful in the
XX CC treatment of infections e.g. meningitis, septic arthritis, and
XX CC endophthalmitis, and inflammation arising from autoimmune disease.
XX SQ Sequence 5 AA:

Query Match 100.0%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
   |||
   2 RTR 4
Db

RESULT 8
AAY23952
ID AAY23952 standard; peptide; 5 AA.
XX
XX AAY23952;
AC
XX
XX 20-MAR-2003 (updated)
DT 22-SEP-1999 (first entry)
XX
XX Peptide inhibiting adhesion between leukocytes and endothelial cells.
DE Adhesion; leukocyte; endothelial cell; bacteria; Bordetella pertussis;
XX

```

KM ciliated respiratory epithelial cell; filamentous haemagglutinin; FHA;
 KM RGD region; cerebral endothelial cell; inflammation; antibiotic therapy;
 KM infection; meningitis; septic arthritis; endophthalmitis.
 XX Synthetic.
 OS
 XX
 PN US932217-A.
 XX
 PD 03-AUG-1999.
 XX
 PF 30-NOV-1994; 94US-0348353.
 XX
 PR 03-MAY-1991; 91US-0695613.
 PR 04-MAY-1992; 92MO-US03725.
 PR 23-MAY-1994; 94US-0247572.
 PR 14-JUL-1994; 94US-0140136.
 XX
 PA (UTRQ) UNIV ROCKEFELLER.
 XX
 PI Masure HR, Tuomanen E;
 XX
 DR WPI: 1999-443571/37.
 XX
 PT Peptides inhibiting the adhesion between leukocytes and endothelial
 PT cells, useful for treating inflammation
 XX
 PS Claim 1: Column 75; 82pp; English.
 XX
 CC The specification describes peptides which inhibit adhesion between
 CC leukocytes and endothelial cells, and peptides which inhibit adhesion
 CC between bacteria (Bordetella pertussis) and ciliated respiratory
 CC epithelial cells. The specification also describes an immunogenic
 CC composition comprising a polypeptide portion of Bordetella pertussis
 CC filamentous haemagglutinin (FHA) containing no RGD region or containing
 CC an amino acid sequence altered in the RGD region, where the polypeptide
 CC portion elicits antibodies which do not cross-react with cerebral
 CC endothelial cells. The peptides and methods are useful for reducing
 CC inflammation during the course of antibiotic therapy of infectious
 CC diseases such as meningitis, septic arthritis, and endophthalmitis.
 CC The present sequence represents a peptide of the invention.
 CC (Updated on 20-MAR-2003 to correct PR field.)
 CC
 SO Sequence 5 AA:
 QY
 DB 1 RTR 3
 III
 2 RTR 4
 DE
 RESULT 9
 ID AAY07209 standard; peptide; 5 AA.
 XX
 AC AAY07209;
 XX
 DT 16-JUL-1999 (first entry)
 XX
 DE Adenoviral NLS peptide #5 for transfection vector.
 XX
 KM Peptide vector; transfection; adenovirus; fiber protein; hydrophobic;
 KM veterinary medicine; gene therapy; antibacterial; anticancer; ribozyme;
 KM human; immunogen; vaccination; antisense; nuclear localisation signal.
 XX
 OS Synthetic.
 OS Adenovirus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /label- Thr, Ala, Ser, Ser-Lys
 FT

XX
 PN FR770537-A1.
 XX
 PD 07-MAY-1999.
 XX
 PF 03-NOV-1997; 97FR-0013771.
 XX
 PR 03-NOV-1997; 97FR-0013771.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 XX
 PI Chroboczek J, Fender P;
 XX
 DR WPI: 1999-290555/25.
 XX
 PT Peptide vector for transfection of cells, containing adenoviral
 PT fiber peptide
 XX
 PS Claim 3; Page 22; 33pp; French.
 XX
 CC The invention relates to a peptide vector for transfection with a
 CC "chemical" comprising, apart from the chemical, at least one
 CC transfection peptide derived, entirely or in part, from an adenoviral
 CC fiber protein and at least one region consisting of at least 50%
 CC hydrophobic amino acids (aa), e.g. Ala, Val, Phe, Ile, Leu, Pro and Met.
 CC The "chemical" is a nucleic acid, protein, peptide or pharmacologically
 CC active agent. The transfection agent is selected from the nuclear
 CC localisation sequences AAY07205-Y07210 and the hydrophobic region from
 CC AAY07211-Y07212. The peptide vectors are used, in human or veterinary
 CC medicine, to treat or prevent diseases, particularly in gene therapy,
 CC e.g. of inherited diseases, viral infections, or as antibacterial and
 CC anticancer agents, also as immunogens for vaccination, where the
 CC "chemical" is nucleic acid, it may encode a therapeutic protein,
 CC antisense sequence or ribozyme.
 CC
 SO Sequence 5 AA:
 QY
 DB 1 RTR 3
 III
 3 RTR 5
 DE
 RESULT 10
 ID AAB21218 standard; peptide; 5 AA.
 XX
 AC AAB21218;
 XX
 DT 23-FEB-2001 (first entry)
 XX
 DE Synthetic complementary peptide.
 XX
 KM Polymorphonuclear leukocyte; PMN; ophthalmological; antiinflammatory;
 KM PMN chemoattractant antagonist; N-acetyl-PGP; N-acetyl-PGX; N-methyl-PGP;
 KM chemically injured eye; inflammatory eye disease; alkali-injured eye;
 XX
 OS Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 5 /note- "C-terminal amide"
 XX
 PN WO200053621-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 08-MAR-2000; 2000MO-US06062.

XX	PR	09-MAR-1999;	99US-0123409.	
XX	XX	(HADDX/) HADDOX J L.		
XX	PA	(BLAL/) BLALOCK J E.		
XX	PA	(PFIS/) PFISTER R R.		
XX	PA	(VILL/) VILLAIN M.		
XX	PI	Haddox J L., Blalock J E., Pfister R R., Villain M;		
XX	DR	WPI; 2000-611433/58.		
XX	PT	Pharmaceutical composition for treating eye diseases, comprises a		
XX	PT	peptide having sequence complementary to a specified sequence -		
XX	PS	Claim 3; Page 36; 42pp; English.		
XX	CC			
XX	CC	The present sequence is a synthetic complementary peptide which is an		
XX	CC	antagonist of the polymorphonuclear leukocyte (PMN) chemottractant,		
XX	CC	N-acetyl-PGP. It is therefore useful for inhibiting PMN polarisation,		
XX	CC	chemotaxis and infiltration into tissue activated by neutrophil		
XX	CC	chemottractant such as N-acetyl-PGP, N-acetyl-PGx, N-methyl-PGP, or		
XX	CC	small peptide chemottractants containing proline and glycine. It may		
XX	CC	be used for treating eye diseases for e.g. alkali-injured eye,		
XX	CC	chemically injured eye and inflammatory eye disease. The present		
XX	CC	sequence is used as a monomer.		
XX	SQ	Sequence 5 AA;		
XX	Query Match	100.0%; Score 15; DB 21; Length 5;		
XX	Best Local Similarity	100.0%; Pred. NO. 9.3e+05;		
XX	Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0.		
OY		1 RTR 3		
Db		1. RTR 3		
RESULT 11				
AAB24246	ID	AAB24246 standard; Peptide; 5 AA.		
XX	XX	AAB24246;		
AC	XX			
XX	DT	08-FEB-2001 (first entry)		
XX	DE	Transport activity peptide #4.		
XX	XX			
XX	KM	Human; telomerase; hTERT; PCR primer; immortalised cell; gene therapy;		
XX	KM	cell therapy; herpes viral VP22 protein; HIV; TAT protein; herpesvirus;		
XX	OS	cell immortalisation activity; telomerase specific activity.		
XX	OS	Herpesvirus.		
XX	XX			
XX	XX	MO200061617-AZ.		
XX	PD	19-OCT-2000.		
XX	XX			
XX	PE	12-APR-2000; 2000MO-US09775.		
XX	XX			
XX	XX	12-APR-1999; 99US-0128893.		
XX	PR	10-APR-2000; 2000US-0546269.		
XX	XX			
XX	XX			
XX	PA	(MODE-) MODEX THERAPEUTQUES SA.		
XX	XX			
XX	PI	Baetge EE, Wong S, Dupraz P, Thorens B;		
XX	DR	WPI; 2000-665115/64.		
XX	XX			
XX	PT	Fusion proteins with cell immortalization and telomerase specific		
XX	PT	activity are useful for increasing replicative capacity of normally		
XX	PT	quiescent cells such as somatic cells to produce cells suitable for		
XX	PT	cell therapy -		

XX Disclosure: Page 12; 40pp; English.

XX

CC The present invention describes a fusion polypeptide (I) comprising

CC polypeptide (Ita) having the transport function of herpes viral VP22

CC protein or HIV Tat protein and polypeptide (Ib) having cell

CC immortalisation activity, telomerase specific activity or telomerase

CC gene activation activity. (1) having (Ib) with cell immortalisation

CC activity is useful for transiently immortalising a cell (C1). (1) having

CC (Ib) with telomerase specific activity is useful for transiently

CC immortalising a cell (C2). Two fusion proteins, with one comprising (Ib)

CC having cell immortalisation activity and other comprising (Ib) having

CC telomerase specific activity are together useful for increasing the

CC replicative activity of a cell (C3) where the cells (C1), (C2) and (C3)

CC are not abundant and are difficult to obtain in pure form in primary

CC culture and includes normal somatic cells suitable for cell therapy,

CC the cells are not permanently immortalising and are not virally infected,

CC but upon removal of the exogenous immortalising or telomerase (I) are

CC suitable for transplantation and use in cell therapy. The present

CC sequence represents a peptide which is used in the exemplification of

CC the present invention.

XX

SQ Sequence 5 AA;

XX

Query Match 100.0%; Score 15; DB 21; Length 5;

Best Local Similarity 100.0%; Pred. NO. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 RTR 3

DB 1 RTR 3

RESULT 12

ID AAY67519

AA67519 standard; peptide; 5 AA.

AC AAY67519;

XX

XX 30-MAY-2000 (first entry)

DE FNA peptide inhibiting leukocyte adhesion to endothelial cells.

XX

KW FNA: blood-brain barrier; filamentous hemagglutinin; endothelial cell;

KW complement C3bi; factor X; integrin receptor CR3; leukocyte migration;

KW bacterial adhesion; brain cancer; acquired immune deficiency syndrome;

KW Parkinson's disease; Alzheimer's disease; antibacterial; anti-epileptic;

KW anti-inflammatory; anticancer; antiviral; antineurodegeneration.

XX

OS Bordetella pertussis.

XX

PN US6015560-A.

XX

PD 18-JAN-2000.

XX

PF 06-JUN-1995; 95US-0465966.

XX

PR 30-NOV-1994; 94US-0348353.

PR 04-MAY-1992; 92MO-US03725.

PR 03-MAY-1991; 91US-0695613.

PR 23-MAY-1994; 94US-0247572.

XX

PA (UYRQ) UNIV ROCKEFELLER.

XX

PI Measure HR, Tuomanen E;

XX

DR WPI; 2000-181133/16.

XX

PT Compositions containing antibody to filamentous hemagglutinin, used

PT e.g. to increase permeability of the blood-brain barrier and to inhibit

PT inflammation or bacterial adhesion -

XX

XX Claim 4; Column 77; 82pp; English.

XX The invention provides a novel pharmaceutical composition for increasing
 CC the permeability of the blood-brain barrier to FHA (filamentous phage). The
 CC composition comprises (1) and an antibody to FHA (filamentous phage).
 CC hemagglutinin) which binds to endothelial cells in brain blood vessels,
 CC increasing permeability. FHA contains polypeptide regions with binding
 CC properties similar to those of complement C3b1, factor X and integrin
 CC receptor CR3, and some anti-FHA antibodies are competitive inhibitors
 CC of these materials, i.e. they reduce leukocyte migration or bacterial
 CC adhesion. The compositions are used to improve delivery of (1) to the
 CC brain, e.g. where (1) is used to treat brain cancer, acquired immune
 CC deficiency syndrome, epilepsy, Parkinson's or Alzheimer's diseases or
 CC other neurological diseases. Other antibodies directed against
 CC particular regions of FHA are used to treat inflammation (caused by
 CC microbial infection or auto-immune diseases), also to prevent adhesion of
 CC Bordetella pertussis to respiratory endothelial cells. Sequences
 CC AA67516-522 represent FHA peptides that inhibit adhesion between
 CC leukocytes and endothelial cells.

XX Sequence 5 AA:

Query Match 100.0%; Score 15; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RTR 3
 |||
 Db 2 RTR 4

RESULT 13

AAE28114
 ID AAE28114 standard: peptide: 5 AA.

XX AAE28114;

DT 13-DEC-2002 (first entry)

DE Human immunoglobulin G1 (IgG1) mutant peptide (residues 385-389) #1.

KW Human: immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;
 KW vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;
 KW immunosuppressive; lymphoid malignancy; respiratory syncytial virus;
 KW anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
 KW virulence; mutant; mutein.

XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT MISC-difference 1 /note- "Wild-type Gly substituted with Arg"

FT MISC-difference 2 /note- "Wild-type Gln substituted with Thr"

FT MISC-difference 3 /note- "Wild-type Pro substituted with Arg"

FT MISC-difference 5 /note- "Wild-type Asn substituted with Pro"

XX WO200260919-A2.

PD 08-AUG-2002.

PF 12-DEC-2001; 2001WO-US48432.

PR 12-DEC-2000; 2000US-254884P.

PR 09-MAY-2001; 2001US-289760P.

XX (MED1-) MEDIMUNE INC.

PA Dall'Acqua W, Johnson LS, Ward ES;

XX WPI, 2002-666925/71.

XX Modified immunoglobulins useful in the treatment of autoimmune
 PT diseases, comprises at least one amino acid modification relative to a
 PT wild-type immunoglobulin constant domain
 XX Example: Page 145, 147pp; English.

XX The invention relates to a modified immunoglobulin (IgG1) which comprises
 CC an IgG constant domain having at least one amino acid modification. The
 CC immunoglobulins are used in the treatment or prevention of a disease or
 CC disorder by passive immunotherapy for vaccinating a subject and for in
 CC vivo diagnosis of a subject. The disease and disorders include a gamma
 CC globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-
 CC host, lymphoid malignancies and passive immunotherapies and also for the
 CC treatment of various systemic infections. The present sequence is human
 CC immunoglobulin G1 (IgG1) mutant peptide (residues 385-389). This peptide
 CC is used in the exemplification of the invention.

XX Sequence 5 AA:

Query Match 100.0%; Score 15; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RTR 3
 |||
 Db 1 RTR 3

RESULT 14

ABB09212
 ID ABB09212 standard: peptide: 5 AA.

XX ABB09212;

DT 08-JUL-2002 (first entry)

DE Glycoprotein cleavage site peptide SEQ ID NO:10.

KW Vaccine; viral infection; immunity; immune response; glycoprotein;
 KW pathogenic virus; HIV; influenza virus; respiratory syncytial virus;
 KW herpes simplex virus; human papilloma virus; Ebola virus; Marburg virus;
 KW hepatitis A virus; hepatitis B virus; hepatitis C virus;
 KW hepatitis D virus; hepatitis E virus.

XX Unidentified.

OS WO200191536-A2.

PD 06-DEC-2001.

PF 04-JUN-2001; 2001WO-US18238.

PR 02-JUN-2000; 2000US-0585599.

XX (GENP-) GENPHAR INC.

PA Wang D;

DR WPI, 2002-122028/16.

XX Replication-competent recombinant virus useful as vaccine for
 PT immunizing humans against pathogenic virus, bacteria and parasites, has
 PT antigens heterologous to the virus and an immuno-stimulator sequence
 XX Example: Page 67; 142pp; English.

XX The present invention describes a replication-competent recombinant
 CC virus (RV) comprising antigen sequences heterologous to RV, each sequence
 CC encoding a bacterial, viral or parasitic antigen whose expression elicits
 CC an immune response against the antigen and cells expressing the antigen
 CC in a host upon infection of host by RV, and an immuno-stimulator (IS)
 CC sequence heterologous to RV. The expression of the IS sequence in the

CC host enhances the immunogenicity of the antigen and RV does not cause a
CC malignancy naturally associated with the pathogen in the host. The RV has
CC virulence, antitubercular, antiparasitic, protozoacide and anti-HIV, and
CC can be used in vaccine production. The RV is useful for enhancing the
CC immunity of a host to one or more pathogenic bacteria such as *Bacillus*
CC *tuberculosis*, *B. anthracis*, *Spiriochetes*, *Borrelia burgdorferi* that causes
CC the Lyme disease in animals, parasites such as malaria, *Cryptosporidium*,
CC *Elmetria*, *Histomonas*, *Leucocytozoon*, *Plasmodium*, *Toxoplasma*, *Trichomonas*,
CC *Leishmania*, *Trypanosoma*, *Giardia*, *Babesia* or *Thelazia*, and pathogenic
CC viruses such as HIV type 1 and type 2, influenza virus, respiratory
CC syncytial virus, herpes simplex virus type 1 and type 2, human papilloma
CC virus, Ebola virus, Marburg virus and hepatitis A, B, C, D and E virus.
CC RV induces a strong and long-lasting immune response to various strains
CC or types of pathogens in the host. The present sequence represents a
CC glycoprotein cleavage site peptide which is given in the exemplification
CC of the present invention.

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OM protein - protein search, using sw model

Run on: September 9, 2003, 23:34:34 ; Search time 28.125 Seconds
(without alignments)
14.646 Million cell updates/sec

Title: US-09-967-003-2

Perfect score: 15

Sequence: 1 RTR 3

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513375 seqs, 137303645 residues

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	3	10	US-09-967-003-2
2	15	100.0	4	10	US-09-736-960-7
3	15	100.0	5	10	US-09-800-433-7
4	15	100.0	5	10	US-09-967-003-3
5	15	100.0	5	12	US-10-286-332A-10
6	15	100.0	5	14	US-10-003-035-10
7	15	100.0	5	15	US-10-212-634-4
8	15	100.0	6	10	US-09-800-433-8
9	15	100.0	6	10	US-09-954-697-54
10	15	100.0	6	10	US-09-990-762-78
11	15	100.0	6	10	US-09-897-107-68
12	15	100.0	6	10	US-09-881-572A-11
13	15	100.0	6	11	US-09-858-852A-78
14	15	100.0	6	11	US-09-500-700-77
15	100.0	6	14	US-10-059-749-17	
					Sequence 2, Appl
					Sequence 7, Appl
					Sequence 7, Appl
					Sequence 3, Appl
					Sequence 10, Appl
					Sequence 10, Appl
					Sequence 4, Appl
					Sequence 8, Appl
					Sequence 54, Appl
					Sequence 78, Appl
					Sequence 68, Appl
					Sequence 11, Appl
					Sequence 78, Appl
					Sequence 77, Appl
					Sequence 17, Appl

16	15	100.0	6	14	US-10-215-297-8	Sequence 8, Appl
17	15	100.0	7	15	US-10-215-298-8	Sequence 8, Appl
18	15	100.0	7	10	US-09-867-852-90	Sequence 90, Appl
19	15	100.0	7	11	US-09-880-748-3182	Sequence 3182, App
20	15	100.0	7	11	US-09-876-904A-498	Sequence 498, App
21	15	100.0	7	12	US-10-271-708-28	Sequence 28, Appl
22	15	100.0	8	11	US-09-876-904A-464	Sequence 464, App
23	15	100.0	9	7	US-08-344-824-37	Sequence 37, Appl
24	15	100.0	9	9	US-09-950-844-13	Sequence 13, Appl
25	15	100.0	9	11	US-09-799-250-16	Sequence 16, Appl
26	15	100.0	9	11	US-09-799-250-23	Sequence 23, Appl
27	15	100.0	9	11	US-09-799-250-31	Sequence 31, Appl
28	15	100.0	9	11	US-09-799-250-34	Sequence 34, Appl
29	15	100.0	9	11	US-09-799-250-40	Sequence 40, Appl
30	15	100.0	9	11	US-09-799-250-130	Sequence 130, App
31	15	100.0	9	11	US-09-799-250-158	Sequence 158, App
32	15	100.0	9	11	US-09-799-250-247	Sequence 247, App
33	15	100.0	9	11	US-09-799-250-331	Sequence 331, App
34	15	100.0	9	11	US-09-799-250-361	Sequence 361, App
35	15	100.0	9	11	US-09-799-250-438	Sequence 438, App
36	15	100.0	9	11	US-09-799-250-443	Sequence 443, App
37	15	100.0	9	11	US-09-799-250-446	Sequence 446, App
38	15	100.0	9	11	US-09-799-250-457	Sequence 457, App
39	15	100.0	9	11	US-09-799-250-456	Sequence 456, App
40	15	100.0	9	11	US-09-799-250-524	Sequence 524, App
41	15	100.0	9	11	US-09-799-250-530	Sequence 530, App
42	15	100.0	9	11	US-09-799-250-536	Sequence 536, App
43	15	100.0	9	11	US-09-799-250-530	Sequence 530, App
44	15	100.0	9	11	US-09-799-250-530	Sequence 530, App
45	15	100.0	9	11	US-09-799-250-536	Sequence 536, App

ALIGNMENTS

RESULT 1

US-09-967-003-2

Sequence 2, Application US/09967/003

Patent No. US20020107202A1

GENERAL INFORMATION:

APPLICANT: Haddox, Jeffrey

APPLICANT: Pfister, Robert

APPLICANT: Blalock, James

APPLICANT: Matteo, Villalain

TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC FILE REFERENCE: 92750/57

CURRENT APPLICATION NUMBER: US/09/967/003

CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: US/09/521,365

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: US 60/123,409

PRIOR FILING DATE: 1999-03-08

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 2

LENGTH: 3

TYPE: PRT

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: description of artificial sequence: amino acid

OTHER INFORMATION: sequence of complementary peptide inhibitor of

OTHER INFORMATION: neutrophils; used as a monomer, dimer, and tetramer

US-09-967-003-2

Query Match

Best Local Similarity 100.0%; Score 15; DB 10; Length 3;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTR 3

Db 1 RTR 3

RESULT 2
US-09-736-960-7
Sequence 7, Application US/09736960
Patent No. US20020102267A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter
APPLICANT: Garman, Jonathan David
APPLICANT: Candia III, Albert Frederick
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: CLASP-5 Transmembrane Protein
FILE REFERENCE: 020054-00051105
CURRENT APPLICATION NUMBER: US/09/736,960
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US 60/160,860
PRIOR FILING DATE: 1999-10-21
PRIOR APPLICATION NUMBER: US 60/162,498
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/170,453
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/182,296
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: US 09/547,276
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,267
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,460
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,527
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,528
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 09/687,837
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,503
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,508
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,539
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,543
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CLASP-5 homolog
OTHER INFORMATION: of furin protease consensus cleavage sequence
US-09-736-960-7
Query Match 100.0%; Score 15; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTR 3
111
DB 2 RTR 4

RESULT 3
US-09-800-433-7
Sequence 7, Application US/09800433
Patent No. US20020106378A1
GENERAL INFORMATION:
APPLICANT: O'Hare and Elliott
TITLE OF INVENTION: Materials and methods for intracellular transport and
FILE REFERENCE: 49408
TITLE OF INVENTION: their uses

CURRENT APPLICATION NUMBER: US/09/800,433
CURRENT FILING DATE: 2000-03-05
PRIOR APPLICATION NUMBER: 09/395,344
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-800-433-7
Query Match 100.0%; Score 15; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTR 3
111
DB 1 RTR 3

RESULT 4
US-09-967-003-3
Sequence 3, Application US/09967003
Patent No. US20020107202A1
GENERAL INFORMATION:
APPLICANT: Haddox, Jeffrey
APPLICANT: Pfister, Robert
APPLICANT: Blalock, James
APPLICANT: Matteo, Villain
TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 92750/57
CURRENT APPLICATION NUMBER: US/09/967,003
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/521,365
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: US 60/123,409
PRIOR FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 5
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: description of artificial sequence: amino acid
OTHER INFORMATION: sequence of complementary peptide inhibitor of
OTHER INFORMATION: neutrophils; used as a monomer
US-09-967-003-3
Query Match 100.0%; Score 15; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
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QY 1 RTR 3
111
DB 1 RTR 3

RESULT 5
US-10-286-332A-10
Sequence 10, Application US/10286332A
Publication No. US20030138459A1
GENERAL INFORMATION:
APPLICANT: Wang, Danher
TITLE OF INVENTION: METHOD OF VACCINATION THROUGH SEROTYPE ROTATION
FILE REFERENCE: 22488-738
CURRENT APPLICATION NUMBER: US/10/286,332A
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US 09/585,599

;; PRIOR FILING DATE: 2000-06-02
;; PRIOR APPLICATION NUMBER: PCT/US01/18238
;; PRIOR FILING DATE: 2001-06-04
;; PRIOR APPLICATION NUMBER: US 10/003,035
;; PRIOR FILING DATE: 2001-11-01
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 10
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Ebola virus
US-10-286-332A-10

Query Match
Best Local Similarity 100.0%; Score 15; DB 12; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
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DB 2 RTR 4

RESULT 6
US-10-003-035-10
;; Sequence 10, Application US/10003035
;; Publication No. US2002015127A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Danher
;; TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
;; FILE REFERENCE: 22488-712
;; CURRENT APPLICATION NUMBER: US/10/003,035
;; PRIOR FILING DATE: 2001-11-01
;; PRIOR APPLICATION NUMBER: 09/585,599
;; PRIOR FILING DATE: 2000-06-02
;; PRIOR APPLICATION NUMBER: PCT/US01/18238
;; PRIOR FILING DATE: 2001-06-04
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 10
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Ebola virus
US-10-003-035-10

Query Match
Best Local Similarity 100.0%; Score 15; DB 14; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
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DB 2 RTR 4

RESULT 7
US-10-212-634-4
;; Sequence 4, Application US/10212634
;; Publication No. US2003011970A1
;; GENERAL INFORMATION:
;; APPLICANT: Lai, Zhenhan
;; APPLICANT: Reiser, Jakob
;; APPLICANT: Brady, Roscoe O.
;; TITLE OF INVENTION: INTERCELLULAR DELIVERY OF A HERPES
;; TITLE OF INVENTION: SIMPLEX VIRUS VP22 FUSION PROTEIN FROM CELLS INFECTED WITH
;; TITLE OF INVENTION: LENTIVIRAL VECTORS
;; FILE REFERENCE: NIH207.001A
;; CURRENT APPLICATION NUMBER: US/10/212,634
;; PRIOR FILING DATE: 2002-08-02
;; PRIOR APPLICATION NUMBER: US 60/310,012
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4
;; LENGTH: 5

;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: sequence motif
US-10-212-634-4

Query Match
Best Local Similarity 100.0%; Score 15; DB 15; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
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DB 1 RTR 3

RESULT 8
US-09-800-433-8
;; Sequence 8, Application US/09800433
;; Patent No. US20020106378A1
;; GENERAL INFORMATION:
;; APPLICANT: O'Hare and Elliott
;; TITLE OF INVENTION: Materials and methods for intracellular transport and
;; TITLE OF INVENTION: their uses
;; FILE REFERENCE: 49408
;; CURRENT APPLICATION NUMBER: US/09/800,433
;; PRIOR FILING DATE: 2000-03-05
;; PRIOR APPLICATION NUMBER: 09/395,344
;; PRIOR FILING DATE: 1999-09-13
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 8
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-800-433-8

Query Match
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
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DB 1 RTR 3

RESULT 9
US-09-954-697-54
;; Sequence 54, Application US/09954697
;; Patent No. US2002010631A1
;; GENERAL INFORMATION:
;; APPLICANT: Alnemri, Emad S.
;; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
;; TITLE OF INVENTION: THEREOF
;; FILE REFERENCE: 480140.431D2
;; CURRENT APPLICATION NUMBER: US/09/954,697
;; PRIOR FILING DATE: 2001-09-14
;; NUMBER OF SEQ ID NOS: 116
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 54
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-09-954-697-54

Query Match
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
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DB 1 RTR 3

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RESULT 10
US-09-990-762-78
; Sequence 78, Application US/09990762
; Patent No. US20020119498A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTW-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/09/990,762
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-990-762-78

Query Match          100.0%; Score 15; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       4 RTR 6

RESULT 11
US-09-897-107-68
; Sequence 68, Application US/09897107
; Patent No. US20020137094A1
; GENERAL INFORMATION:
; APPLICANT: IMAGISHI, AKIHIKO
; TITLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HAVING
; FILE REFERENCE: 2103830S0
; CURRENT APPLICATION NUMBER: US/09/897,107
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: JP2000-201920
; PRIOR FILING DATE: 2000-07-04
; PRIOR APPLICATION NUMBER: JP2001-164332
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-897-107-68

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Db       1 RTR 3

RESULT 12
US-09-881-572A-11
; Sequence 11, Application US/09881572A

; Patent No. US20020164583A1
; GENERAL INFORMATION:
; APPLICANT: Roth, Monica;
; APPLICANT: Bupp, Keith;
; APPLICANT: University of Medicine and Dentistry of New Jersey
; TITLE OF INVENTION: Targeting Viral Vectors to Specific Cells
; FILE REFERENCE: 601-1-095
; CURRENT APPLICATION NUMBER: US/09/881,572A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/212,239
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Rat Leukemia Virus
US-09-881-572A-11

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       3 RTR 5

RESULT 13
US-09-858-852A-78
; Sequence 78, Application US/09858852A
; Publication No. US20030044787A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTW-030.01 (20021-3001)
; CURRENT APPLICATION NUMBER: US/09/858,852A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-858-852A-78

Query Match          100.0%; Score 15; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTR 3
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Db       4 RTR 6

RESULT 14
US-09-500-700-77
; Sequence 77, Application US/09500700
; Publication No. US20030059767A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: BARBAS III, Carlos F.
; APPLICANT: GOTTESFELD, Joel M.
; APPLICANT: WRIGHT, Peter E.
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
; FILE REFERENCE: SCRIP1160-4
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				Indels
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RESULT 15
 US-10-059-749-17
 Sequence 17, Application US/10059749
 Publication No. US20020183504A1
 GENERAL INFORMATION:
 APPLICANT: Ainemri, Emad S.
 Fernandez-Ainemri, Teresa
 Litnack, Gerald
 TITLE OF INVENTION: Apoptotic Protease Mcb6, Nucleic Acids
 Encoding Same and Methods of Use
 NUMBER OF SEQUENCES: 87
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/059,749
 FILING DATE: 29-Jan-2002
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/865,579
 FILING DATE: 29-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-ID 2180
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-9849
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

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; ; TOPOLOGY: linear  
; ; MOLECULE TYPE: peptide  
; ; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
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Db            1 RTR 3
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Search completed: September 9, 2003, 23:47:27
Job time : 29.125 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2003, 23:31:48 ; Search time 213 Seconds

(without alignments)
12.816 Million cell updates/sec

Title: US-09-967-003-2

Perfect score: 15
Sequence: 1 RRR 3

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Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Pending Patents AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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					Sequence 2, Appl1

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7	15 <td>100.0</td> <td>4</td> <td>17</td> <td>US-09-340-852-61</td> <td>Sequence 61, Appl</td>	100.0	4	17	US-09-340-852-61	Sequence 61, Appl
8	15 <td>100.0</td> <td>4</td> <td>17</td> <td>US-09-340-852-68</td> <td>Sequence 68, Appl</td>	100.0	4	17	US-09-340-852-68	Sequence 68, Appl
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26	15 <td>100.0</td> <td>5</td> <td>28</td> <td>US-10-212-634-4</td> <td>Sequence 4, Appl1</td>	100.0	5	28	US-10-212-634-4	Sequence 4, Appl1
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36	15 <td>100.0</td> <td>6</td> <td>17</td> <td>US-09-308-441-9</td> <td>Sequence 9, Appl1</td>	100.0	6	17	US-09-308-441-9	Sequence 9, Appl1
37	15 <td>100.0</td> <td>6</td> <td>21</td> <td>US-09-500-700-77</td> <td>Sequence 77, Appl</td>	100.0	6	21	US-09-500-700-77	Sequence 77, Appl
38	15 <td>100.0</td> <td>6</td> <td>21</td> <td>US-09-746-731-17</td> <td>Sequence 17, Appl</td>	100.0	6	21	US-09-746-731-17	Sequence 17, Appl
39	15 <td>100.0</td> <td>6</td> <td>23</td> <td>US-09-800-433-8</td> <td>Sequence 8, Appl1</td>	100.0	6	23	US-09-800-433-8	Sequence 8, Appl1
40	15 <td>100.0</td> <td>6</td> <td>23</td> <td>US-09-858-852A-78</td> <td>Sequence 78, Appl</td>	100.0	6	23	US-09-858-852A-78	Sequence 78, Appl
41	15 <td>100.0</td> <td>6</td> <td>23</td> <td>US-09-881-572A-11</td> <td>Sequence 11, Appl</td>	100.0	6	23	US-09-881-572A-11	Sequence 11, Appl
42	15 <td>100.0</td> <td>6</td> <td>23</td> <td>US-09-897-107-68</td> <td>Sequence 68, Appl</td>	100.0	6	23	US-09-897-107-68	Sequence 68, Appl
43	15 <td>100.0</td> <td>6</td> <td>25</td> <td>US-09-950-083-4229</td> <td>Sequence 4229, Ap</td>	100.0	6	25	US-09-950-083-4229	Sequence 4229, Ap
44	15 <td>100.0</td> <td>6</td> <td>25</td> <td>US-09-950-083B-4229</td> <td>Sequence 4229, Ap</td>	100.0	6	25	US-09-950-083B-4229	Sequence 4229, Ap
45	15 <td>100.0</td> <td>6</td> <td>25</td> <td>US-09-954-697-54</td> <td>Sequence 54, Appl</td>	100.0	6	25	US-09-954-697-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
PCT-US00-06062-2
Sequence 2, Application PC/TUS0006062
GENERAL INFORMATION:
APPLICANT: Haddox, Jeffrey Lynn
APPLICANT: Bialock, James Edwin
APPLICANT: Pfister, Roswell Robert
APPLICANT: Villain, Matteo
TITLE OF INVENTION: Synthetic Complementary Peptides and
FILE REFERENCE: D6201PCT
CURRENT APPLICATION NUMBER: PCT/US00/06062
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: US 60/123,409
EARLIER FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 2
LENGTH: 3
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: amino acid sequence of complementary peptide
OTHER INFORMATION: inhibitor of neutrophils; used as monomer
OTHER INFORMATION: dimer and tetramer

PCT-US00-06062-2

Query Match 100.0%; Score 15; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
DB 1 RTR 3

RESULT 2
US-09-967-003-2

Sequence 2, Application US/09967003
GENERAL INFORMATION:
APPLICANT: Haddox, Jeffrey
APPLICANT: Pilster, Robert
APPLICANT: Blalock, James
APPLICANT: Matteo, Viliain
TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC
FILE REFERENCE: 92750/57
CURRENT APPLICATION NUMBER: US/09/967,003
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/521,365
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: US 60/123,409
PRIOR FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 3
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: description of artificial sequence: amino acid
OTHER INFORMATION: sequence of complementary peptide inhibitor of
OTHER INFORMATION: neutrophils; used as a monomer, dimer, and tetramer
US-09-967-003-2

Query Match 100.0%; Score 15; DB 25; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
DB 1 RTR 3

RESULT 3
PCT-US97-12974A-61

Sequence 61, Application PC/TUS9712974A
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/12974A

FILING DATE: 23 Jul 97

CLASSIFICATION:

PRIOR APPLICATION DATA: US 08/685,589

APPLICATION NUMBER: 24-JUL-1996

FILING DATE: 24-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 8067-026-228

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-9741

TELEX: 66141

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..4

OTHER INFORMATION: /product= "Beta-turn"

PCT-US97-12974A-61

Query Match 100.0%; Score 15; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
DB 1 RTR 3

RESULT 4

PCT-US97-12974A-68

Sequence 68, Application PC/TUS9712974A
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/12974A
FILING DATE: 23 Jul 97
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/685,589
FILING DATE: 24-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 68:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-12974A-68

Query Match      100.0%; Score 15; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 RTR 3
      |||
DB      2 RTR 4

RESULT 5
PCT-US97-19557-61
; Sequence 61, Application PC/TUS9719557
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/19557
; FILING DATE: herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-19557-61

Query Match      100.0%; Score 15; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 RTR 3
      |||
DB      2 RTR 4
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```

DB      1 RTR 3

RESULT 6
PCT-US97-19557-68
; Sequence 68, Application PC/TUS9719557
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/19557
; FILING DATE: herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-048-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-19557-68

Query Match      100.0%; Score 15; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 RTR 3
      |||
DB      2 RTR 4

RESULT 7
US-09-340-852-61
; Sequence 61, Application US/09340852
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
```

COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,852
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589
FILING DATE: 24-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: Not Relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..4
OTHER INFORMATION: /product= "beta-turn"
US-09-340-852-61

Query Match 100.0%; Score 15; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
Db 1 RTR 3

RESULT 8
US-09-340-852-68
Sequence 68, Application US/09340852
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,852
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589
FILING DATE: 24-JUL-1996

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: Not Relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..4
OTHER INFORMATION: /product= "Beta-turn"
US-09-340-852-68

Query Match 100.0%; Score 15; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
Db 2 RTR 4

RESULT 9
US-09-736-960-7
Sequence 7, Application US/09736960
GENERAL INFORMATION:
APPLICANT: Lu, Peter
APPLICANT: Garman, Jonathan David
APPLICANT: Candia III, Albert Frederick
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: CLASP-5 Transmembrane Protein
FILE REFERENCE: 020054-000511US
CURRENT APPLICATION NUMBER: US/09/736,960
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US 60/160,860
PRIOR FILING DATE: 1999-10-21
PRIOR APPLICATION NUMBER: US 60/162,498
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/170,453
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/182,296
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: US 09/547,276
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,267
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,460
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,527
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,528
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 09/687,837
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,503
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,508
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,539
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,543
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 134

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CLASP-5 homolog
US-09-736-960-7

Query Match
Best Local Similarity 100.0%; Score 15; DB 21; Length 4;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RTR 3
Db 2 RTR 4

RESULT 10
US-10-031-289-1758
Sequence 1758, Application US/10031289
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: MASIGNANI Vega
APPLICANT: SCARLATO Vincenzo
APPLICANT: SCARSELLI Maria
APPLICANT: GALEOTTI Cesira
TITLE OF INVENTION: ANTIGENIC MENINGOCOCCAL PEPTIDES
FILE REFERENCE: P022260MO
CURRENT APPLICATION NUMBER: US/10/031,289
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: GB-9916529.2
PRIOR FILING DATE: 1999-07-14
NUMBER OF SEQ ID NOS: 1769
SOFTWARE: SeqMln99, version 1.02
SEQ ID NO 1758
LENGTH: 4
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-10-031-289-1758

Query Match
Best Local Similarity 100.0%; Score 15; DB 26; Length 4;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RTR 3
Db 2 RTR 4

RESULT 11
PCT-US00-06062-3
Sequence 3, Application PC/TUS0006062
GENERAL INFORMATION:
APPLICANT: Haddox, Jeffrey Lynn
APPLICANT: Blalock, James Edwin
APPLICANT: Pfister, Roswell Robert
APPLICANT: Villalón, Matteo
TITLE OF INVENTION: Synthetic Complementary Peptides and
FILE REFERENCE: D6201PCT
CURRENT APPLICATION NUMBER: PCT/US00/06062
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: US 60/123,409
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3
LENGTH: 5
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: amino acid sequence of complementary peptide

OTHER INFORMATION: Inhibitor of neutrophils; used as monomer
PCT-US00-06062-3

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RTR 3
Db 1 RTR 3

RESULT 12
PCT-US01-48432-105
Sequence 105, Application PC/TUS0148432
GENERAL INFORMATION:
APPLICANT: MEDIMUNE, INC.
TITLE OF INVENTION: MOLECULES WITH EXTENDED HALF-LIVES, COMPOSITIONS AND USES THE
FILE REFERENCE: 10271-027-228
CURRENT APPLICATION NUMBER: PCT/US01/48432
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/254,884
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/238,760
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 105
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-48432-105

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RTR 3
Db 1 RTR 3

RESULT 13
PCT-US02-30251-51
Sequence 51, Application PC/TUS0230251
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as represented by
APPLICANT: Secretary,
APPLICANT: Health and Human Services
APPLICANT: NABEL, GARY
APPLICANT: YANG, ZHI-YONG
APPLICANT: SULLIVAN, NANCY
APPLICANT: SANCHEZ, ANTHONY
TITLE OF INVENTION: Development of a Preventive Vaccine for
FILE REFERENCE: NIH221.001PCT
CURRENT APPLICATION NUMBER: PCT/US02/30251
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US 60/326476
PRIOR FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 5
TYPE: PRT
ORGANISM: Ebola Virus
PCT-US02-30251-51

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RTR 3

Db 111
2 RTR 4

RESULT 14

PCT-US02-35112-10
Sequence 10: Application PC/TUS0235112
GENERAL INFORMATION:
APPLICANT: Wang, Danher
TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
FILE REFERENCE: 22488-740
CURRENT APPLICATION NUMBER: PCT/US02/35112
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 09/585,599
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US01/18238
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: US 10/003,035
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 5
TYPE: PRT
ORGANISM: Ebola virus
PCT-US02-35112-10

Query Match 100.0%; Score 15; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
Db 2 RTR 4

RESULT 15

US-08-247-572-8
Sequence 8: Application US/08247572
GENERAL INFORMATION:
APPLICANT: Tucumanen, Elaine
APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wyatt, Gerber, Burke and Badie
STREET: 645 Madison Avenue, 5th Floor
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,572
FILING DATE: 23-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US92/03725 PCT
FILING DATE: 04-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,613
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Burke, Henry T.
REGISTRATION NUMBER: 18,975
REFERENCE/DOCKET NUMBER: 18367A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-826-0171

TELEFAX: 212-755-6256
TELEX: 421733GEDRIG
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-247-572-8

Query Match 100.0%; Score 15; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
Db 2 RTR 4

Search completed: September 9, 2003, 23:45:43
Job time : 215 secs

GenCore version 5.1.6
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OH protein - protein search, using sw model

Run on: September 9, 2003, 23:32:23 ; Search time 6.375 Seconds
(without alignments)
4.496 Million cell updates/sec

Title: US-09-967-003-2

Perfect score: 15

Sequence: 1 RTR 3

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 47124 seqs, 9554045 residues

Total number of hits satisfying chosen parameters: 47124

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	9	US-09-291-417D-118	Sequence 118, App
2	15	100.0	9	US-09-561-107-8	Sequence 8, App1
3	15	100.0	9	US-09-799-250B-16	Sequence 16, App1
4	15	100.0	9	US-09-799-250B-23	Sequence 23, App1
5	15	100.0	9	US-09-799-250B-31	Sequence 31, App1
6	15	100.0	9	US-09-799-250B-34	Sequence 34, App1
7	15	100.0	9	US-09-799-250B-40	Sequence 40, App1
8	15	100.0	9	US-09-799-250B-130	Sequence 130, App
9	15	100.0	9	US-09-799-250B-158	Sequence 158, App
10	15	100.0	9	US-09-799-250B-247	Sequence 247, App
11	15	100.0	9	US-09-799-250B-331	Sequence 331, App
12	15	100.0	9	US-09-799-250B-349	Sequence 349, App
13	15	100.0	9	US-09-799-250B-361	Sequence 361, App
14	15	100.0	9	US-09-799-250B-438	Sequence 438, App
15	15	100.0	9	US-09-799-250B-443	Sequence 443, App
16	15	100.0	9	US-09-799-250B-444	Sequence 444, App
17	15	100.0	9	US-09-799-250B-446	Sequence 446, App
18	15	100.0	9	US-09-799-250B-456	Sequence 456, App
19	15	100.0	9	US-09-799-250B-457	Sequence 457, App
20	15	100.0	9	US-09-799-250B-524	Sequence 524, App
21	15	100.0	9	US-09-799-250B-530	Sequence 530, App
22	15	100.0	9	US-09-799-250B-536	Sequence 536, App
23	15	100.0	9	US-09-799-250B-540	Sequence 540, App
24	15	100.0	9	US-09-799-250B-551	Sequence 551, App
25	15	100.0	9	US-09-799-250B-552	Sequence 552, App
26	15	100.0	9	US-09-799-250B-552	Sequence 552, App

27	15	100.0	9	US-09-799-250B-563	Sequence 563, App
28	15	100.0	9	US-09-799-250B-620	Sequence 620, App
29	15	100.0	9	US-09-799-250B-640	Sequence 640, App
30	15	100.0	9	US-09-799-250B-641	Sequence 641, App
31	15	100.0	9	US-09-799-250B-652	Sequence 652, App
32	15	100.0	9	US-09-799-250B-662	Sequence 662, App
33	15	100.0	10	US-09-291-417D-83	Sequence 83, App1
34	15	100.0	10	US-09-799-250B-65	Sequence 65, App1
35	15	100.0	10	US-09-799-250B-76	Sequence 76, App1
36	15	100.0	10	US-09-799-250B-80	Sequence 80, App1
37	15	100.0	10	US-09-799-250B-93	Sequence 93, App1
38	15	100.0	10	US-09-799-250B-185	Sequence 185, App
39	15	100.0	10	US-09-799-250B-198	Sequence 198, App
40	15	100.0	10	US-09-799-250B-274	Sequence 274, App
41	15	100.0	10	US-09-799-250B-277	Sequence 277, App
42	15	100.0	10	US-09-799-250B-369	Sequence 369, App
43	15	100.0	10	US-09-799-250B-392	Sequence 392, App
44	15	100.0	10	US-09-799-250B-403	Sequence 403, App
45	15	100.0	10	US-09-799-250B-409	Sequence 409, App

ALIGNMENTS

```
RESULT 1
US-09-291-417D-118
Sequence 118, Application US/09291417D
GENERAL INFORMATION:
APPLICANT: PLOMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
TITLE OF INVENTION: STEE20-RELATED PROTEIN KINASES
FILE REFERENCE: 036602/0329
CURRENT APPLICATION NUMBER: US/09/291,417D
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/081,784
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 118
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-291-417D-118

Query Match      100.0%; Score 15; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 RTR 3
      III
Db      7 RTR 9

RESULT 2
US-09-561-107-8
Sequence 8, Application US/09561107
GENERAL INFORMATION:
APPLICANT: Kahn, Michael
APPLICANT: Ogibu, Cyprian O.
APPLICANT: Eguchi, Masakatsu
APPLICANT: Kim, Hwa-OK
APPLICANT: Boatman, Patrick Douglas Jr.
TITLE OF INVENTION: BETA-SHEET METRICS AND USE THEREOF AS
FILE REFERENCE: 670063.413D3
CURRENT APPLICATION NUMBER: US/09/561,107
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
```

ORGANISM: UNKNOWN
FEATURE:
OTHER INFORMATION: Class MCH I peptides - Influenza nucleoprotein
US-09-561-107-8

Query Match 100.0%; Score 15; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
DB 4 RTR 6

RESULT 3
US-09-799-250B-16
Sequence 16, Application US/09799250B
GENERAL INFORMATION:
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Paris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 12IP1: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01 (511582003400)
CURRENT APPLICATION NUMBER: US/09/799,250B
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250B-16

Query Match 100.0%; Score 15; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
DB 7 RTR 9

RESULT 4
US-09-799-250B-23
Sequence 23, Application US/09799250B
GENERAL INFORMATION:
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Paris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 12IP1: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01 (511582003400)
CURRENT APPLICATION NUMBER: US/09/799,250B
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250B-23

Query Match 100.0%; Score 15; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
DB 5 RTR 7

RESULT 5
US-09-799-250B-31
Sequence 31, Application US/09799250B
GENERAL INFORMATION:
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Paris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 12IP1: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01 (511582003400)
CURRENT APPLICATION NUMBER: US/09/799,250B
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250B-31

Query Match 100.0%; Score 15; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
DB 6 RTR 8

RESULT 6
US-09-799-250B-34
Sequence 34, Application US/09799250B
GENERAL INFORMATION:
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Paris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 12IP1: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01 (511582003400)
CURRENT APPLICATION NUMBER: US/09/799,250B
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250B-34

Query Match 100.0%; Score 15; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
DB 4 RTR 6

```
RESULT 7
US-09-799-250B-40
; Sequence 40, Application US/09799250B
; GENERAL INFORMATION:
; APPLICANT: Pia M. Chailita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.34US01 (511582003400)
; CURRENT FILING DATE: 2003-07-14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-250B-40

Query Match
Best Local Similarity 100.0%; Score 15; DB 5; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
    |||
Db 7 RTR 9

RESULT 8
US-09-799-250B-130
; Sequence 130, Application US/09799250B
; GENERAL INFORMATION:
; APPLICANT: Pia M. Chailita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.34US01 (511582003400)
; CURRENT FILING DATE: 2003-07-14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-250B-130

Query Match
Best Local Similarity 100.0%; Score 15; DB 5; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
    |||
Db 6 RTR 8

RESULT 9
US-09-799-250B-158
; Sequence 158, Application US/09799250B
; GENERAL INFORMATION:
; APPLICANT: Pia M. Chailita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
```

```
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Faris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01 (511582003400)
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 158
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250B-158

Query Match
Best Local Similarity 100.0%; Score 15; DB 5; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
    |||
Db 6 RTR 8

RESULT 10
US-09-799-250B-247
; Sequence 247, Application US/09799250B
; GENERAL INFORMATION:
; APPLICANT: Pia M. Chailita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.34US01 (511582003400)
; CURRENT FILING DATE: 2003-07-14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 247
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-250B-247

Query Match
Best Local Similarity 100.0%; Score 15; DB 5; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
    |||
Db 4 RTR 6

RESULT 11
US-09-799-250B-331
; Sequence 331, Application US/09799250B
; GENERAL INFORMATION:
; APPLICANT: Pia M. Chailita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.34US01 (511582003400)
```

```

; CURRENT APPLICATION NUMBER: US/09/799,250B
; CURRENT FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 331
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-250B-331
```

```

Query Match          100.0%; Score 15; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 RTR 3
        |||
Db       4 RTR 6
```

```

RESULT 12
; Sequence 349, Application US/09799250B
; GENERAL INFORMATION:
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Paris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 121PFI: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.34US01 (511582003400)
; CURRENT APPLICATION NUMBER: US/09/799,250B
; CURRENT FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 349
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-250B-349
```

```

Query Match          100.0%; Score 15; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 RTR 3
        |||
Db       7 RTR 9
```

```

RESULT 13
; Sequence 361, Application US/09799250B
; GENERAL INFORMATION:
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Paris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 121PFI: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.34US01 (511582003400)
; CURRENT APPLICATION NUMBER: US/09/799,250B
; CURRENT FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 361
; LENGTH: 9
; TYPE: PRT
```

```

; ORGANISM: Homo sapiens
US-09-799-250B-361
```

```

Query Match          100.0%; Score 15; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 RTR 3
        |||
Db       1 RTR 3
```

```

RESULT 14
; Sequence 438, Application US/09799250B
; GENERAL INFORMATION:
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Paris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 121PFI: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.34US01 (511582003400)
; CURRENT APPLICATION NUMBER: US/09/799,250B
; CURRENT FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 438
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-250B-438
```

```

Query Match          100.0%; Score 15; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 RTR 3
        |||
Db       6 RTR 8
```

```

RESULT 15
; Sequence 443, Application US/09799250B
; GENERAL INFORMATION:
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Paris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 121PFI: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.34US01 (511582003400)
; CURRENT APPLICATION NUMBER: US/09/799,250B
; CURRENT FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 443
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-250B-443
```

```

Query Match          100.0%; Score 15; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 RTR 3
111
Db 2 RTR 4

Search completed: September 9, 2003, 23:46:05
Job time : 6.375 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 9, 2003, 23:28:28 ; Search time 18.75 Seconds
(without alignments)
15.387 Million cell updates/sec

Title: US-09-967-003-2

Perfect score: 15
Sequence: 1 RTR 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	2	A28497 neurotensin-related
2	15	100.0	20	2	PC4385 GroEL protein homo
3	15	100.0	20	2	PC4386 GroEL protein homo
4	15	100.0	22	2	PN0070 hypothetical prote
5	15	100.0	23	2	S35694 cystic fibrosis tr
6	15	100.0	25	1	R6B748 ribosomal protein
7	15	100.0	26	2	S64715 formin binding pro
8	15	100.0	26	2	S33869 ribosomal protein
9	15	100.0	27	2	I51989 streptomycin 3 - E
10	15	100.0	29	2	T34643 hypothetical prote
11	15	100.0	30	1	CLHR22 protamine XII - Pa
12	15	100.0	30	1	CLHR22 gene CYP112 prote
13	15	100.0	30	2	I52254 cystic fibrosis tr
14	15	100.0	30	2	S48114 S56757
15	15	100.0	31	2	S56757 link protein - hum
16	15	100.0	31	2	B98020 N-acetylneuraminat
17	15	100.0	31	2	B98020 N-acetylneuraminat
18	15	100.0	32	2	D61014 defensin NP-1 - ra
19	15	100.0	32	2	I51089 protamine - Japane
20	15	100.0	32	2	T36275 hypothetical prote
21	15	100.0	33	2	A87213 hypothetical prote
22	15	100.0	33	2	A58533 CD41 homolog - cha
23	15	100.0	34	2	S20439 protamine yellow
24	15	100.0	34	2	A85974 hypothetical prote
25	15	100.0	35	2	T48890 cytidin-7 - mouse
26	15	100.0	35	2	S18224 filamentous hemagg
27	15	100.0	36	2	H48110 RNA recognition mo
28	15	100.0	36	2	F84791 hypothetical prote
29	15	100.0	36	2	G81853 hypothetical prote

30	15	100.0	37	2	S03941 hydrogen dehydroge
31	15	100.0	37	2	G95010 hypothetical prote
32	15	100.0	37	2	E97596 hypothetical prote
33	15	100.0	38	2	D55543 Tnp protein - Pseu
34	15	100.0	38	2	T20493 hypothetical prote
35	15	100.0	38	2	G71305 probable ribosomal
36	15	100.0	39	2	G90716 promoter RNA (limpo
37	15	100.0	39	2	S13496
38	15	100.0	39	2	A48544 neurotensin-related
39	15	100.0	39	2	G64801
40	15	100.0	40	2	S26797 hypothetical prote
41	15	100.0	40	2	B82382 Ig heavy chain V r
42	15	100.0	40	2	I45887 elastin - bovine (
43	15	100.0	41	2	B87687 hypothetical prote
44	15	100.0	41	2	D72350 hypothetical prote
45	15	100.0	42	2	C45495 beta-defensin-3 -

ALIGNMENTS

RESULT 1
A28497
neurotensin-related protein - turkey (fragment)
C:Species: Melalegris gallapavo (common turkey)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 23-May-1997
C:Accession: A28497
R:Carraway, R.E.; Cochran, D.E.; Ruane, S.E.
J. Biol. Chem. 262, 15886-15889, 1987
A:Title: Isolation, structures, and biologic activity of neurotensin-related peptide
A:Reference number: A28497; MUID:88058942; PMID:2445741
A:Accession: A28497
A:Molecule type: protein
A:Residues: 1-15 <CAP>
C:Superfamily: collagen alpha 3(VI) chain; animal kunitz-type proteinase inhibitor h
C:Keywords: neuropeptide

Query Match
Best Local Similarity 100.0%; Score 15; DB 2; Length 15;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
|||
Db 8 RTR 10

RESULT 2
PC4385
GroEL protein homolog - Pseudomonas sp. (fragment)
N:Alternate names: molecular chaperone
C:Species: Pseudomonas sp.
C:Date: 06-Nov-1997 #sequence_revision 06-Nov-1997 #text_change 07-May-1999
R:Tokunaga, M.; Matsunaka, K.; Tokunaga, H.
Biosci. Biotechnol. Biochem. 61, 1388-1390, 1997
A:Title: Identification and NH2-terminal amino acid sequences of DnaK and GroEL homo
A:Reference number: PC4383; MUID:97446535; PMID:9301123
A:Accession: PC4385
A:Molecule type: protein
A:Residues: 1-20 <YOK>
A:Experimental source: strain 21-Na
C:Comment: This protein plays a role in protein folding.

Query Match
Best Local Similarity 100.0%; Score 15; DB 2; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
|||
Db 12 RTR 14

RESULT 3

PC4386
GroEL protein homolog - *Acinetobacter* sp. (fragment)
N:Alternate names: molecular chaperone
C:Species: *Acinetobacter* sp.
C>Date: 06-Nov-1997 #sequence_revision 06-Nov-1997 #text_change 07-May-1999
C:Accession: PC4386
R:Tokunaga, M.; Matsuno, K.; Tokunaga, H.
Biosci. Biotechnol. Biochem. 61, 1368-1390, 1997
A:Title: Identification and NH2-terminal amino acid sequences of DnaK and GroEL homologs
A:Reference number: PC4383; MUID:97446535; PMID:9301123
A:Accession: PC4386
A:Molecule type: protein
A:Residues: 1-20 <TOK>
A:Experimental source: strain 204-1
C:Comment: This protein plays a role in protein folding.

Query Match 100.0%; Score 15; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
DB 12 RTR 14

RESULT 4
PT0070
hypothetical protein (gffc 3' region) - *Streptococcus* mutans (fragment)
C:Species: *Streptococcus* mutans
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 18-Jun-1993
C:Accession: PT0070
R:Jeda, S.; Shiroza, T.; Kuramitsu, H.K.
Gene 69, 101-109, 1998
A:Title: Sequence analysis of the gffc gene from *Streptococcus* mutans GS-5.
A:Reference number: JT0345; MUID:89137980; PMID:2976010
A:Accession: PT0070
A:Molecule type: DNA
A:Residues: 1-22 <UED>
A:Experimental source: strain GS-5

Query Match 100.0%; Score 15; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
DB 13 RTR 15

RESULT 5
S35694
cyclic fibrosis transmembrane conductance regulator - human (fragment)
C:Species: *Homo sapiens* (man)
C>Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 28-May-1999
C:Accession: S35694
R:Mele, C.A.; Serra, C.; Stoyanova, V.; Aguzzoli, C.; Faraguna, D.; Tamandl, A.; Bertoni
FEBS Lett. 329, 159-162, 1993
A:Title: Alternative splicing of a previously unidentified CFTR exon introduces an in-frame
A:Reference number: S35693; MUID:93359040; PMID:7689062
A:Accession: S35694
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-23 <MEU>
A:Cross-references: GB:S64699; NID:9408285; PIDN:AAB27879.1; PID:9408286

Query Match 100.0%; Score 15; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
DB 6 RTR 8

RESULT 6
R6BYAB
ribosomal protein L41.e, cytosolic - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein D1290; protein YDL133c-a; protein YDL184c; ribosomal prote
C:Species: *Saccharomyces cerevisiae*
C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Sep-2000
C:Accession: S22246; S22247; S11264; S58733; S67739; S78073
R:Suuki, K.; Hashimoto, T.; Otake, E.
Curr. Genet. 17, 185-190, 1990
A:Title: Yeast ribosomal proteins: XI. Molecular analysis of two genes encoding YL41,
A:Reference number: S22246; MUID:90254826; PMID:2187623
A:Accession: S22246
A:Molecule type: DNA
A:Residues: 1-25 <SUO>
A:Cross-references: EMBL:X16066; GSPDB:GN00004; MIPS:YDL133c-a; NID:94819; PIDN:CAA34
A:Genetics: RPL47B
A:Accession: S22247
A:Molecule type: DNA
A:Residues: 1-25 <SUA>
A:Cross-references: EMBL:X16065; GSPDB:GN00004; MIPS:YDL184c; NID:94817; PIDN:CAA342C
R:Otake, E.; Higo, K.I.; Itoh, T.
Mol. Gen. Genet. 195, 544-546, 1984
A:Title: Yeast ribosomal proteins. VIII. Isolation of two proteins and sequence chara
A:Reference number: S11249
A:Accession: S11264
A:Molecule type: protein
A:Residues: 1-25 <ORR>
R:Verhaaselt, P.; Voet, M.; Volckaert, G.
Yeast 11, 961-966, 1995
A:Title: New open reading frames, one of which is similar to the nlfv gene of *Azotoba*
A:Reference number: S58730; MUID:96021607; PMID:8533471
A:Accession: S58733
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-25 <VER>
A:Cross-references: EMBL:X83276; NID:91004294; PIDN:CAA58262.1; PID:91004310
A:Genetics: RPL47A
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1994
R:Volckaert, G.; Verhaaselt, P.; Voet, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67735
A:Accession: S67739
A:Molecule type: DNA
A:Residues: 1-25 <VOL>
A:Cross-references: EMBL:Z74232; GSPDB:GN00004; MIPS:YDL184c; NID:91431298; PIDN:CAA5
A:Experimental source: strain S288C
A:Genetics: RPL47A
R:Saluz, H.P.; Koefl, S.; Hanemann, V.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67677
A:Accession: S78073
A:Molecule type: DNA
A:Residues: 1-25 <SAL>
A:Cross-references: EMBL:Z74181; NID:91431202; PIDN:CAA98705.1; PID:91903289; GSPDB:G
A:Genetics: RPL47B
A:Genetics: <RPL47B>
A:Gene: SGD:RPL47B; YL18B; MIPS:YDL133c-a
A:Cross-references: MIPS:YDL133c-a; SGD:S0002293
A:Map position: 4L
C:Genetics: <RPL47A>
A:Gene: SGD:RPL47A; YL11A; MIPS:YDL184c
A:Cross-references: MIPS:YDL184c; SGD:S0002343
A:Map position: 4L
C:Superfamily: rat ribosomal protein L41
C:Keywords: protein biosynthesis; ribosome
F:1-25/Product: ribosomal protein L41.e #status experimental <MAT>

Query Match 100.0%; Score 15; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
Db 9 RTR 11

RESULT 7

S64715
formin binding protein 23 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 23-Sep-2002
C:Accession: S64715
R:Chan, D.C.; Bedford, M.T.; Leder, P.
EMBO J. 15, 1045-1054, 1996
A:Title: Formin binding proteins bear WWP/MM domains that bind proline-rich peptides and
A:Reference number: S64711; MUID:96183189; PMID:8605874
A:Accession: S64715
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-26 <CHN>
A:Cross-references: EMBL:U40748; NID:91255026; PIDN:NA52476.1; PID:91255027
C:Superfamily: formin binding protein; MM repeat homology
F:1-26/Domain: MM repeat homology (fragment) <MM1>

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
Db 17 RTR 19

RESULT 8

S33869
ribosomal protein Thx - Thermus aquaticus
N:Alternate names: Ribosomal protein TS21
C:Species: Thermus aquaticus
C:Date: 22-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 07-May-1999
C:Accession: S33869; S33870; S33871; S51072
R:Choli, T.; Franceschi, F.; Yonath, A.; Wittmann-Liebold, B.
Biol. Chem. Hoppe-Seyler 374, 377-383, 1993
A:Title: Isolation and characterization of a new ribosomal protein from the thermophilic
A:Reference number: S33869; MUID:93363224; PMID:8357533
A:Accession: S33869
A:Molecule type: protein
A:Residues: 1-26 <CHO>
A:Note: the source is designated as Thermus thermophilus
A:Accession: S33870
A:Molecule type: protein
A:Residues: 1-26 <CHM>
A:Note: the source is designated as Thermus flavus
A:Accession: S33871
A:Molecule type: protein
A:Residues: 1-26 <CHF>
R:Tsiiboli, P.; Herfurth, E.; Choli, T.
Eur. J. Biochem. 226, 169-177, 1994
A:Title: Purification and characterization of the 30S ribosomal proteins from the bacter
A:Reference number: S51053; MUID:95045586; PMID:7957245
A:Accession: S51072
A:Molecule type: protein
A:Residues: 1-26 <ST>
A:Note: the source is designated as Thermus thermophilus
C:Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
Db 6 RTR 8

RESULT 9

151989
streptomycin 3 - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 03-Jun-2002
C:Accession: 151989; S26613
R:Bito, A.; Susani, M.
Antimicrob. Agents Chemother. 38, 1172-1175, 1994
A:Title: Revised analysis of aadA gene of plasmid pSA.
A:Reference number: 151989; MUID:94346828; PMID:7915099
A:Accession: 151989
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-27 <RES>
A:Cross-references: EMBL:X68227; NID:949135; PIDN:CAA48307.1; PID:949136
C:Genetics:
A:Gene: aacA
C:Keywords: nucleotidyltransferase

Query Match 100.0%; Score 15; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
Db 22 RTR 24

RESULT 10

T34643
hypothetical protein SC10H5.05 SC10H5.05 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T34643
R:Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z21550
A:Accession: T34643
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-29 <OLI>
A:Cross-references: EMBL:AL031232; PIDN:CAA20277.1; GSPDB:GNO0070; SCODDB:SC10H5.05
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCODDB:SC10H5.05

Query Match 100.0%; Score 15; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
111
Db 22 RTR 24

RESULT 11

CLHRV2
protamine YII - Pacific herring
N:Alternate names: clupeine
C:Species: Clupea pallasii, Clupea harengus pallasii (Pacific herring)
C:Date: 12-Aug-1981 #sequence_revision 12-Aug-1981 #text_change 16-Feb-1997
C:Accession: A38052; A02677
R:Suzuki, K.; Ando, T.
J. Biochem. 72, 1419-1432, 1972
A:Title: Studies on protamines. XVI. The complete amino acid sequence of clupeine YI.
A:Reference number: A38052; MUID:73223106; PMID:4664740
A:Accession: A38052
A:Molecule type: protein
A:Residues: 1-30 <SUZ>
C:Superfamily: protamine Y2
C:Keywords: chromosomal protein; DNA binding; spermatogenesis

Query Match 100.0%; Score 15; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
|||
Db 4 RTR 6

RESULT 12

CLHR2A
protamine VII - Atlantic herring
N:Alternate names: Clupeine
C:Species: Clupea harengus, Clupea harengus harengus (Atlantic herring)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Feb-1997
C:Accession: A37575; A02677
R:Chang, W.J.; Nukushina, M.; Ishii, S.; Nakahara, C.; Ando, T.
submitted to the Atlas, August 1970
A:Reference number: A37575
A:Accession: A37575
A:Molecule type: Protein
A:Residues: 1-30 <CHA>
C:Superfamily: protamine Y2
C:Keywords: chromosomal protein; DNA binding; spermatogenesis

Query Match 100.0%; Score 15; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
|||
Db 4 RTR 6

RESULT 13

gene CYP11B2 protein - rat (fragment)
I52254
C:Species: Rattus sp. (rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Mar-1999
C:Accession: I52254
R:Nakai, K.; Imai, M.; Shimada, H.; Okada, Y.; Ogishima, T.; Ishimura, Y.
Biochem. Biophys. Res. Commun. 180, 1187-1193, 1991
A:Title: Structural differences in 5'-flanking regions of rat cytochrome P-450a1d and F
A:Reference number: I52254; M01D:92062142; PMID:1953771
A:Accession: I52254
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-30 <RES>
A:Cross-references: GB:S63898; M1D:9238626
C:Genetics:
A:Gene: CYP11B2
C:Superfamily: human cytochrome P450 CYP11B1; cytochrome P450 homology
C:Keywords: heme; transmembrane protein

Query Match 100.0%; Score 15; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
|||
Db 20 RTR 22

RESULT 14

S48114
cystic fibrosis transmembrane conductance regulator - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 07-May-1999
C:Accession: S48114
R:Trezise, A.E.O.; Buchwald, M.; Higgins, C.F.
Hum. Mol. Genet. 2, 801-802, 1993
A:Title: Testis-specific, alternative splicing of rodent CFTR mRNA.
A:Reference number: S48114; M01D:93357755; PMID:7689012
A:Accession: S48114

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-30 <TRE>
A:Cross-references: EMBL:X72693

Query Match 100.0%; Score 15; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
|||
Db 12 RTR 14

RESULT 15

S56757
link protein - human
C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C:Accession: S56757
R:Rhodes, C.; Yamada, Y.
Nucleic Acids Res. 23, 2305-2313, 1995
A:Title: Characterization of a glucocorticoid responsive element and identification c
A:Reference number: S56756; M01D:9534387; PMID:7610060
A:Accession: S56757
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-31 <RHO>
A:Cross-references: EMBL:X55056
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1991

Query Match 100.0%; Score 15; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
|||
Db 29 RTR 31

Search completed: September 9, 2003, 23:35:21
Job time : 21.75 secs


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CC -----
DR EMBL: X16065; CAA34201.1; -
DR EMBL: X16066; CAA34202.1; -
DR EMBL: X83276; CAA58262.1; -
DR EMBL: 274232; CAA98759.1; -
DR EMBL: 274181; CAA98705.1; -
DR EMBL: 274182; CAA98706.1; -
DR EMBL: X96876; CAA6526.1; -
DR PIR: S22246; R6BY4B.
DR SGD: S0002343; RPL1A.
DR Pfam: PF05162; Ribosomal L41.
KM Ribosomal protein; Multigene family.
SQ SEQUENCE 25 AA: 3337 MW; BD2629DD9ED85381 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
Db 9 RTR 11

RESULT 2
RSHX_THETH STANDARD; PRT; 26 AA.
AC P32193; P80383; Q9F2A8;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein Thx.
GN RPSU.
OS Thermus thermophilus, and
OS Thermus aquaticus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274, 271;
RN [1]
RP MEDLINE-93363224; Pubmed-8357533;
RX Choi T., Franceschi F., Yonath A., Wittmann-Liebold B.;
RT "Isolation and characterization of a new ribosomal protein from the
RT thermophilic eubacteria, Thermus thermophilus, T. aquaticus and T.
RT flavus.";
RL Biol. Chem. Hoppe-Seyler 374:377-383(1993).
RN [2]
RP SEQUENCE.
RC SPECIES-T. thermophilus;
RC STRAIN-HB8 / ATCC 27634;
RX MEDLINE-95045586; Pubmed-7957245;
RA Tsaloli P., Herfurth E., Choi T.;
RT "Purification and characterization of the 30S ribosomal proteins from
RT the bacterium Thermus thermophilus.";
RL Eur. J. Biochem. 226:169-177(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-T. thermophilus; STRAIN-HB8 / ATCC 27634;
RX MEDLINE-21421773; Pubmed-11530930;
RA Leontidou F., Triantafyllidou D., Choi-Papadopoulos T.;
RT "On the characterization of the putative 520-thx operon of Thermus
RT thermophilus.";
RL Biol. Chem. 382:1001-1006(2001).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (3.05 ANGSTROMS) OF THE 30S SUBUNIT.
RC SPECIES-T. thermophilus;
RX MEDLINE-20466110; Pubmed-11014182;
RA Wimberly B.T., Brodersen D.E., Clemens W.M. Jr., Morgan-Warren R.J.,
RA Carter A.P., Vornhagen C., Hartsch T., Ramakrishnan V.;
RT "Structure of the 30S ribosomal subunit.";
RL Nature 407:327-339(2000).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS) OF THE 30S SUBUNIT.
RC SPECIES-T. thermophilus;
RX MEDLINE-21097713; Pubmed-11163189;
RA Brodersen D.E., Clemens W.M. Jr., Carter A.P., Morgan-Warren R.J.,
RA Wimberly B.T., Ramakrishnan V.;
RT "The structural basis for the action of the antibiotics tetracycline,
RT pactamycin, and hygromycin B on the 30S ribosomal subunit.";
RL Cell 103:1143-1154(2000).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (3.00 ANGSTROMS) OF THE 30S SUBUNIT.
RC SPECIES-T. thermophilus;
RX MEDLINE-20466111; Pubmed-11014183;
RA Carter A.P., Clemens W.M. Jr., Brodersen D.E., Morgan-Warren R.J.,
RA Wimberly B.T., Ramakrishnan V.;
RT "Functional insights from the structure of the 30S ribosomal subunit
RT and its interactions with antibiotics.";
RL Nature 407:340-348(2000).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (5.00 ANGSTROMS) OF THE RIBOSOME.
RC SPECIES-T. thermophilus;
RX MEDLINE-21402420; Pubmed-11511350;
RA Yusupova G.Z., Yusupov M.M., Cate J.H.D., Noller H.F.;
RT "The path of messenger RNA through the ribosome.";
RL Cell 106:233-241(2001).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF THE 30S SUBUNIT.
RC SPECIES-T. thermophilus; STRAIN-HB27;
RX MEDLINE-21192023; Pubmed-11296217;
RA Pioletti M., Schluenzen F., Harms J., Zariwach R., Gluehmann M.,
RA Avila H., Bashan A., Bartels H., Bartels T., Jacobi C., Hartsch T.,
RA Yonath A., Franceschi F.;
RT "Crystal structures of complexes of the small ribosomal subunit with
RT tetracycline, edeine and IF3.";
RL EMBO J. 20:1829-1839(2001).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF THE 30S SUBUNIT.
RC SPECIES-T. thermophilus;
RX MEDLINE-21119514; Pubmed-1128145;
RA Carter A.P., Clemens W.M. Jr., Brodersen D.E., Morgan-Warren R.J.,
RA Hartsch T., Wimberly B.T., Ramakrishnan V.;
RT "Crystal structure of an initiation factor bound to the 30S ribosomal
RT subunit.";
RL Science 291:498-501(2001).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (5.5 ANGSTROMS) OF THE RIBOSOME.
RC SPECIES-T. thermophilus;
RX MEDLINE-21238793; Pubmed-11283358;
RA Yusupov M.M., Yusupova G.Z., Baucum A., Lieberman K., Earnest T.N.,
RA Cate J.H.D., Noller H.F.;
RT "Crystal structure of the ribosome at 5.5 A resolution.";
RL Science 292:883-896(2001).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (3.11 ANGSTROMS) OF THE 30S SUBUNIT.
RC SPECIES-T. thermophilus;
RX MEDLINE-21238794; Pubmed-11340196;
RA Ogile J.M., Brodersen D.E., Clemens W.M. Jr., Tarry M.J., Carter A.P.,
RA Ramakrishnan V.;
RT "Recognition of cognate transfer RNA by the 30S ribosomal subunit.";
RL Science 292:897-902(2001).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (3.05 ANGSTROMS) OF THE 30S SUBUNIT.
RC SPECIES-T. thermophilus;
RX MEDLINE-21856772; Pubmed-11866529;
RA Brodersen D.E., Clemens W.M. Jr., Carter A.P., Wimberly B.T.,
RA Ramakrishnan V.;
RT "Crystal structure of the 30S ribosomal subunit from Thermus
RT thermophilus: structure of the proteins and their interactions with
RT 16S RNA.";
RL J. Mol. Biol. 316:725-768(2002).
CC -I- FUNCTION: Binds at the top of the head of the 30S subunit. It
CC stabilizes a number of different RNA elements and thus is
CC important for subunit structure.
CC -I- SUBUNIT: Part of the 30S ribosomal subunit.
CC -I- SIMILARITY: BELONGS TO THE S31E FAMILY OF RIBOSOMAL PROTEINS.

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CC CC -1- DATABASE: NAME-T. thermophilus 30S ribosomal subunit structure;
CC WWW-http://afl.mrc-lmb.cam.ac.uk/ribc/30S/'.
CC -----
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CC -----
CC DR EMBL: AJ295159; CAC15068.1; -
CC DR PIR: S33869; S33869.
CC DR PDB: 1FJG; 25-SEP-00.
CC DR PDB: 1HR0; 24-JAN-01.
CC DR PDB: 1HNW; 21-FEB-01.
CC DR PDB: 1HNZ; 21-FEB-01.
CC DR PDB: 1I94; 12-APR-01.
CC DR PDB: 1I95; 12-APR-01.
CC DR PDB: 1I96; 12-APR-01.
CC DR PDB: 1I97; 12-APR-01.
CC DR PDB: 1IGX; 01-JUN-01.
CC DR PDB: 1IHK; 04-MAY-01.
CC DR PDB: 1IBL; 04-MAY-01.
CC DR PDB: 1IBM; 04-MAY-01.
CC DR PDB: 1JG0; 14-SEP-01.
CC DR PDB: 1JGP; 14-SEP-01.
CC DR PDB: 1JGQ; 14-SEP-01.
CC DR PDB: 1LIU; 22-MAR-02.
CC DR PDB: 1JSE; 12-APR-02.
CC FT Ribosomal protein; rRNA-binding; rRNA-binding; 3D-structure.
CC KW INT. MET.
CC SO SEQUENCE 26 AA; 3206 MW; 8582641145D8C604 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RTR 3
Db 6 RTR 8

RESULT 3
PRT1_CLUPA STANDARD; PRT; 30 AA.
ID PRT1_CLUPA
AC P02335;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Protamine YII (Clupeine YII).
OS Clupea pallasii (Pacific herring), and
OC Clupea harengus (Atlantic herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
OC Clupea.
CC NCBI_TaxID=30724, 7950;
CC [1]
CC RP SEQUENCE.
CC RC SPECIES=C. pallasii;
CC RX MEDLINE=73223106; PubMed=4664740;
CC RA Suzuki K., Ando T.;
CC RT 'Studies on protamines. XVI. The complete amino acid sequence of
CC clupeine YII.';
CC RL J. Biochem. 72:1419-1432(1972).
CC [2]
CC RP SEQUENCE.
CC RC SPECIES=C. harengus;
CC RA Chang W.J., Nakashima M., Ishii S., Nakahara C., Ando T.;
CC Submitted (AUG-1970) to the FIR data bank.
CC -1- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

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CC CC -1- SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC CC -1- SUBCELLULAR LOCATION: Nuclear.
CC CC -1- TISSUE SPECIFICITY: Testis.
CC -----
CC DR PIR: A37575; C1HR2A.
CC DR PIR: A38052; C1HR2.
CC KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
CC Tests; DNA condensation; Nuclear protein.
CC SO SEQUENCE 30 AA; 4049 MW; 7F9BB80F3ADA566 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RTR 3
Db 4 RTR 6

RESULT 4
PRT_ORYLA STANDARD; PRT; 32 AA.
ID PRT_ORYLA
AC Q91185;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protamine.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.
CC NCBI_TaxID=8090;
CC [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Orange-red; TISSUE=Testis;
CC RA Tamura M., Yamamoto H., Onitake K.;
CC RT 'Cloning of protamine cDNA of the medaka (Oryzias latipes) and its
CC expression during spermatogenesis.';
CC RL Dev. Growth Differ. 36:419-425(1994).
CC -1- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Testis.
CC -----
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CC -----
CC DR EMBL: D63796; BAA09865.1; -
CC DR PIR: I51089; I51089.
CC KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
CC Tests; DNA condensation; Nuclear protein.
CC SO SEQUENCE 32 AA; 4220 MW; E10EC3A5B2ED6803 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RTR 3
Db 17 RTR 19

RESULT 5
TAT_SIVM2 STANDARD; PRT; 32 AA.
ID TAT_SIVM2
AC P05912;
DT 01-NOV-1988 (Rel. 09, Created)

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DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Simian immunodeficiency virus (Wm251 isolate) (SIV-MAC).
OC Viruses: Retroviridae; Lentivirus.
OX NCBI_TaxID=11734.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86122665; PubMed=2893293;
RA Kestler H.M., Li Y., Naidu Y.M., Butler C.V., Ochs M.F., Jaenel G.,
RA King N.W., Daniel M.D., Desrosiers R.C.;
RT *Comparison of simian immunodeficiency virus isolates.*;
RL Nature 331:619-622(1988).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- MISCELLANEOUS: THIS IS A MACAOE ISOLATE.
CC -----
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CC -----
CC EMBL: X06879; -; NOT_ANNOTATED_CDS.
DR HIV: X06879; JAT5M251.
KM Transcription regulation; Activator; RNA-binding; Nuclear protein;
KM AIDS.
FT NON_TER 1 1
SQ SEQUENCE 32 AA: 3556 MW: 211547CBE6F4D817 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
DB 6 RTR 8

RESULT 6
Y50A_MYCTU STANDARD; PRT; 33 AA.
AC 09CB56;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein Rv0500.1/ML2428.1.
GN Rv0500.1 OR Rv0500B OR MT0521.1 OR ML2428.1 OR ML2428A.
OS Mycobacterium tuberculosis, and
OS Mycobacterium leprae.
OC Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1769;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98293987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Badcock S.V., Eigmeier K., Bow S., Barry C.E. III, Tekala F.,
RA Gordon R., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skellon S., Squares S., Squares R.,
RA Skellon J.E., Taylor K., Whitehead S., Barrell B.G.;
RT *Deciphering the biology of Mycobacterium tuberculosis from the

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RT complete genome sequence.*;
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2118732; PubMed=11234002;
RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holtroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skellon J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT *Massive gene decay in the leprosy bacillus.*;
RL Nature 409:1007-1011(2001).
CC -----
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CC -----
CC EMBL: Z77162; -; NOT_ANNOTATED_CDS.
DR EMBL: AE006953; -; NOT_ANNOTATED_CDS.
DR PIR: A87213; A87213.
DR Leproma; ML2428A; -;
DR TIGR: MT0521.1; -;
DR Tuberculist; Rv0500B; -;
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 33 AA: 4145 MW: 8156A587F16291F5 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
DB 23 RTR 25

RESULT 7
PRT_DICLA STANDARD; PRT; 34 AA.
AC 09PS27;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Proteinae.
OS Dientarchus labrax (European sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OX NCBI_TaxID=13489;
RN [1]
RP SEQUENCE.
RT TISSUE=Sperm;

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RA MEDLINE-93139742; PubMed-8423442;
 RA Saperas N., Ribes E., Buena C., Garcia-Hegart F., Chiva M.;
 RT "Differences in chromatin condensation during spermatogenesis in two
 RT species of fish with distinct protamines.";
 RL J. Exp. Zool. 265:185-194(1993).
 CC -1- FUNCTION: PROTEIN SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
 CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
 CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: Testis.
 CC Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
 KW Testis; DNA condensation; Nuclear protein.
 SO SEQUENCE 34 AA; 4565 MW; EEPF41CB25D10DE CRC64;

Query Match 100.0%; Score 15; DB 1; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 |||
 DB 16 RTR 18

RESULT 8
 ID PRT_PERFV STANDARD; PRT; 34 AA.
 AC P29629;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE Protamine.
 OS Perca flavescens (Yellow perch).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Percidae; Perca.
 OX NCBI_Taxid-8167;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-92183928; PubMed-1544489;
 RA Chao H., Davies P.L.;
 RT "Amino acid sequence of the unique protamine from yellow perch.";
 RL FEBS Lett. 299:166-168(1992).
 CC -1- FUNCTION: PROTEIN SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
 CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
 CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: Testis.
 CC PIR: S20439; S20439.
 DR Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
 KW Testis; DNA condensation; Nuclear protein.
 SO SEQUENCE 34 AA; 4552 MW; EEPF4E0F87C6B2DE CRC64;

Query Match 100.0%; Score 15; DB 1; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 |||
 DB 16 RTR 18

RESULT 9
 ID HOXF_RHOOP STANDARD; PRT; 37 AA.
 AC P22658;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE NAD-reducing hydrogenase hoxs alpha subunit (EC 1.12.1.2) (Fragment).
 OS HOXF.
 OS Rhodococcus opacus (Nocardia opaca).
 SO Plasmid.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Nocardiaceae; Rhodococcus.
 OX NCBI_Taxid-37919;
 RN [1]
 RP SEQUENCE.
 RC STRAIN-1B;
 RX MEDLINE-89231684; PubMed-2496982;
 RA Zaborosch C., Schneider K., Schlegel H.G., Kratzin H.;
 RT "Comparison of the NH2-terminal amino acid sequences of the four non-
 RT identical subunits of the NAD-linked hydrogenases from Nocardia opaca
 RT 1b and Alicyclobacillus glutinosus H16.";
 RL Eur. J. Biochem. 181:175-180(1989).
 CC -1- FUNCTION: SUBUNIT ALPHA AND GAMMA OF HOXS CONSTITUTE AN NADH--
 CC OXIDOREDUCTASE.
 CC -1- CATALYTIC ACTIVITY: H(2) + NAD(+) = H(+) + NADH.
 CC -1- COFACTOR: Binds 1 FMN and 1 4Fe-4S cluster (Potential).
 CC -1- SUBUNIT: TETRAMER OF AN ALPHA AND A GAMMA SUBUNIT (FLAVIN-
 CC CONTAINING DIMER), AND A DELTA AND A NICKEL-CONTAINING BETA
 CC SUBUNIT (HYDROGENASE DIMER).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 51 kDa SUBUNIT FAMILY.
 DR InterPro: IPR002023; Complex_24kDa.
 DR InterPro: IPR001949; Complex_51k.
 DR ProDom: PD003859; Complex_24kDa; 1.
 DR PROSITE: PS00644; COMPLEX1_51K_1; PARTIAL.
 DR PROSITE: PS00645; COMPLEX1_51K_2; PARTIAL.
 KW Oxidoreductase; Flavoprotein; FMN; Metal-binding; Iron-sulfur; Iron;
 KW 4Fe-4S; NAD; Plasmid.
 FT NOL_TER 37
 SO SEQUENCE 37 AA; 4273 MW; 5A1C36E8B866C9D CRC64;

Query Match 100.0%; Score 15; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 |||
 DB 15 RTR 17

RESULT 10
 ID NPF_HELAS STANDARD; PRT; 39 AA.
 AC P41321;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neuropeptide F (NPF).
 OS Helix aspersa (Brown garden snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigamurethra; Helicoidea; Helicidae; Helix.
 OX NCBI_Taxid-6535;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Circumoesophageal ganglion;
 RX MEDLINE-93087780; PubMed-1472265;
 RA Leung P.S., Shaw C., Maule A.G., Thim L., Johnston C.F., Irvine G.B.;
 RT "The primary structure of neuropeptide F (NPF) from the garden snail,
 RT Helix aspersa.";
 RL Regul. Pept. 41:71-81(1992).
 CC -1- FUNCTION: MAY HAVE AN IMPORTANT PHYSIOLOGICAL ROLE IN
 CC NEUROREGULATION.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: NEURONAL SOMATA AND FIBERS.
 CC -1- SIMILARITY: Belongs to the NPY family.
 DR PIR: A48544; A48544.
 DR InterPro: IPR001955; Pancreatic_horm.
 DR Pfam: PF00159; hormones; 1.
 DR SMART: SM00309; PAH; 1.
 DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS50276; PANCREATIC_HORMONE_2; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 39 39 AMIDATION.

SO SEQUENCE 39 AA: 4855 MW; 4B54AA7414CAAE33 CRC64;
 Query Match 100.0%; Score 15; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 111
 36 RTR 38

DB 22 RTR 24

RESULT 11
 BD02_BOVIN STANDARD; PRT: 40 AA.
 AC P46160;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Beta-defensin 2 (BNDB-2) (BNDB-2).
 GN DEF82.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE.
 RC STRAIN=Hereford; TISSUE=Neutrophils;
 RX MEDLINE=93203264; PubMed=8454635;
 RA Selsted M.E., Tang Y.-O., Morris W.L., McGuire P.A., Novotny M.J.,
 RA Smith W., Henschen A.H., Cullor J.S.;
 RT Purification, primary structures, and antibacterial activities of
 RT beta-defensins, a new family of antimicrobial peptides from bovine
 RT neutrophils.;
 RT J. Biol. Chem. 268:6641-6648(1993).
 CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY. ACTIVE AGAINST E. COLI ML35
 CC AND S. AUREUS 502A.
 CC -1- TISSUE SPECIFICITY: NEUTROPHILIC GRANULES.
 CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
 CC PIR: C45495; C45495.
 DR HSSP: P46170; 1BNB.
 DR InterPro: IPR001855; Defensin_beta.
 DR InterPro: IPR006080; Defensin_mammal.
 DR Pfam: PF00711; Defensin_beta; 1.
 DR SMART: SM00048; DEFSN; 1.
 KW Antibiotic.
 FT DISULFID 7 36 BY SIMILARITY.
 FT DISULFID 14 29 BY SIMILARITY.
 FT DISULFID 19 37 BY SIMILARITY.
 SQ SEQUENCE 40 AA: 4649 MW; 9DD6B4E125CEBE30 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 111
 22 RTR 24

DB 22 RTR 24

RESULT 12
 BD06_BOVIN STANDARD; PRT: 42 AA.
 AC P46164;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Beta-defensin 6 (BNDB-6) (BNDB-6).
 GN DEF6.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE.
 RC STRAIN=Hereford; TISSUE=Neutrophils;
 RX MEDLINE=93203264; PubMed=8454635;
 RA Selsted M.E., Tang Y.-O., Morris W.L., McGuire P.A., Novotny M.J.,
 RA Smith W., Henschen A.H., Cullor J.S.;
 RT Purification, primary structures, and antibacterial activities of
 RT beta-defensins, a new family of antimicrobial peptides from bovine
 RT neutrophils.;
 RT J. Biol. Chem. 268:6641-6648(1993).
 CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY. ACTIVE AGAINST E. COLI ML35
 CC AND S. AUREUS 502A.
 CC -1- TISSUE SPECIFICITY: NEUTROPHILIC GRANULES.
 CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
 CC PIR: P45495; P45495.
 DR HSSP: P46170; 1BNB.
 DR InterPro: IPR001855; Defensin_beta.
 DR InterPro: IPR006080; Defensin_mammal.
 DR Pfam: PF00711; Defensin_beta; 1.
 DR SMART: SM00048; DEFSN; 1.
 KW Antibiotic; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 9 38 BY SIMILARITY.
 FT DISULFID 16 31 BY SIMILARITY.
 FT DISULFID 21 39 BY SIMILARITY.
 SQ SEQUENCE 42 AA: 4839 MW; C9E8E9B20DAEB97 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 111
 24 RTR 26

DB 24 RTR 26

RESULT 13
 RL34_BRUME STANDARD; PRT: 44 AA.
 AC O81DA1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L34.
 GN RPLM OR BMEI0276 OR BRA1021.
 OS Brucella melitensis, and
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459; 29461;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC SPECIES=B. melitensis; STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RX DelVecchio V.G., Kapatal V., Redkar R.J., Patra G., Mufier C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Telleson J.-O.,
 RA Haselkorn R., Kyriades N., Overbeek R.;
 RT The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis.;
 RT Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B. suis; STRAIN=1330 / Biovar 1;
 RX MEDLINE=2247741; PubMed=12271122;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., Debey R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J., Van Aken S.E.,
 RA Richmond S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
 RA Hoover D.L., Lindler L.E., Hailing S.M., Boyle S.M., Fraser C.M.;

RT "The Brucella suis genome reveals fundamental similarities between
 animal and plant pathogens and symbionts."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AE009666; AA153518.1; -
 DR EMBL: AE014595; AA034189.1; -
 DR PIR: AC3544; AC3544.
 DR TIGR: BRA1021; -
 DR HAMAP: MF_00391; -; 1.
 DR InterPro: IPR000271; Ribosomal_L34.
 DR Pfam: PF00468; Ribosomal_L34; 1.
 DR ProDom: PD003101; Ribosomal_L34; 1.
 DR TIGRFAMs: TIGR01030; rpmh_bact; 1.
 DR PROSITE: PS00784; RIBOSOMAL_L34; 1.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 44 AA; 5168 MW; 71548DBBF75DE274 CRC64;
 Query Match 100.0%; Score 15; DB 1; Length 44;
 Best Local Similarity 100.0%; Pred. No. 1,8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RTR 3
 DB 35 RTR 37
 RESULT 14
 RL34_LISMO STANDARD; PRT; 44 AA.
 ID 092603;
 AC 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 50S ribosomal protein L34.
 GN RPHM OR LMO2856 OR LIN2988.
 OS Listeria monocytogenes, and
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1639, 1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES: L.monocytogenes, and L.innocua;
 RC STRAIN: BGE- / Serovar 1/2a, and CLIP 11262 / Serovar 6a;
 RA MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Depoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussinget O.,
 RA Elian K.-D., Fsihl H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Gebel M., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kieft J., Kuhn M., Kunst F., Kurapkai H.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nodtsek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
 RA Varguez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of Listeria species."
 RL Science 294:849-852(2001).
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AL591984; CAD01069.1; -
 DR EMBL: AL596174; CAC98213.1; -
 DR PIR: AE1805; AE1805.
 DR PIR: AG1431; AG1431.
 DR Listlist: LMO2988; -
 DR Listlist: LMO2856; -
 DR HAMAP: MF_00391; -; 1.
 DR InterPro: IPR000271; Ribosomal_L34.
 DR Pfam: PF00468; Ribosomal_L34; 1.
 DR ProDom: PD003101; Ribosomal_L34; 1.
 DR TIGRFAMs: TIGR01030; rpmh_bact; 1.
 DR PROSITE: PS00784; RIBOSOMAL_L34; 1.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 44 AA; 5299 MW; BC4B3C97DDC7B49 CRC64;
 Query Match 100.0%; Score 15; DB 1; Length 44;
 Best Local Similarity 100.0%; Pred. No. 1,8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RTR 3
 DB 19 RTR 21
 RESULT 15
 RL34_CHLPN STANDARD; PRT; 45 AA.
 ID 0926X1; 09J080;
 AC 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 50S ribosomal protein L34.
 GN RPHM OR RL34 OR CPN0935 OR CP0926.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN: CWL029;
 RC MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."
 RL Nat. Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN: AR39;
 RC MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Kouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson M., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MOPn and Chlamydia
 RT pneumoniae AR39."
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN: J138;
 RC MEDLINE=20330349; PubMed=10871362;
 RA Shira T., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kihara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA."
 RL Nucleic Acids Res. 28:2311-2314(2000).
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CC -----
DR EMBL: AE001673; AAD19073.1; -;
DR EMBL: AE002251; AAF38710.1; -;
DR EMBL: AP002548; BAA9143.1; -;
DR PIR: A72017; A72017;
DR PIR: E86607; E86607;
DR TIGR: CP0926; -;
DR HAMAP: MF_00391; -; 1.
DR InterPro: IPR000271; Ribosomal_L34.
DR Pfam: PF00468; Ribosomal_L34; 1.
DR ProDom: PD003101; Ribosomal_L34; 1.
DR TIGRPFAM: TIGR01030; rpmh_bact; 1.
DR PROSITE: PS00784; RIBOSOMAL_L34; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 45 AA; 5548 MW; 1F91D87C8343E0D CRC64;

Query Match 100.0%; Score 15; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
|||
Db 19 RTR 21

Search completed: September 9, 2003, 23:32:15
Job time : 11.5 secs

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OM protein - protein search, using sw model

Run on: September 9, 2003, 23:28:08 ; Search time 45 Seconds

(Without alignments)
17.204 Million cell updates/sec

Title: US-09-967-003-2

Sequence: 1 RTR 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	8	019961	019961 gossypium d
2	15	100.0	8	019958	019958 gossypium d
3	15	100.0	8	019960	019960 gossypium t
4	15	100.0	8	019959	019959 gossypium m
5	15	100.0	8	019956	019956 gossypium a
6	15	100.0	9	08MEM3	08mem3 howittia tr
7	15	100.0	10	087617	087617 sida hooker
8	15	100.0	11	08MEM7	08mem7 lagunaria p
9	15	100.0	11	08MEM2	08mem2 abelmoschus
10	15	100.0	11	08MEM5	08mem5 abelmoschus
11	15	100.0	11	08MEM0	08mem0 hibiscus pe
12	15	100.0	11	08MEM8	08mem8 dombeya tll
13	15	100.0	11	08MEM1	08mem1 alyogyne pl
14	15	100.0	11	08MEM3	08mem3 hibiscus no
15	15	100.0	11	08MEM7	08mem7 hibiscus dr
16	15	100.0	11	08MEM9	08mem9 pavonia has

17	15	100.0	11	8	08MEM0	08mem0 hibiscus co
18	15	100.0	11	8	08MEM3	08mem3 alyogyne cr
19	15	100.0	11	8	08MEM5	08mem5 hibiscus ml
20	15	100.0	11	8	08MEM1	08mem1 hibiscus ca
21	15	100.0	11	8	08MEM7	08mem7 fiorta viti
22	15	100.0	12	8	08MEM4	08mem4 hibiscus nl
23	15	100.0	12	8	08MEM5	08mem5 hibiscus en
24	15	100.0	12	8	08MEM3	08mem3 hibiscus wa
25	15	100.0	12	8	08MEM4	08mem4 hibiscus sc
26	15	100.0	12	8	08MEM0	08mem0 gossypium s
27	15	100.0	12	8	08MEM1	08mem1 hibiscus in
28	15	100.0	12	8	08MEM6	08mem6 malva negle
29	15	100.0	12	8	08MEM1	08mem1 malva negle
30	15	100.0	12	8	08MEM8	08mem8 alyogyne hu
31	15	100.0	12	8	08MEM2	08mem2 hibiscus me
32	15	100.0	12	8	08MEM7	08mem7 hibiscus sa
33	15	100.0	12	8	08MEM5	08mem5 decaschisti
34	15	100.0	12	8	08MEM9	08mem9 hibiscus tr
35	15	100.0	12	8	08MEM6	08mem6 hibiscus pe
36	15	100.0	12	8	08MEM1	08mem1 hibiscus fr
37	15	100.0	12	8	08MEM0	08mem0 malvaicus
38	15	100.0	12	8	08MEM4	08mem4 hibiscus pe
39	15	100.0	12	8	08MEM0	08mem0 hibiscus he
40	15	100.0	12	8	08MEM2	08mem2 hibiscus br
41	15	100.0	12	8	08MEM0	08mem0 hibiscus t
42	15	100.0	12	8	08MEM3	08mem3 hibiscus bu
43	15	100.0	12	8	08MEM6	08mem6 hibiscus ti
44	15	100.0	12	8	08MEM2	
45	15	100.0	12	8	08MEM7	

ALIGNMENTS

RESULT 1
ID 019961 PRELIMINARY; PRT; 8 AA.
AC 019961;
DT 01-JAN-1998 (TREMELREL, 05, Created)
DT 01-JAN-1998 (TREMELREL, 05, Last sequence update)
DT 01-DEC-2001 (TREMELREL, 19, Last annotation update)
DE Ribosomal protein L16 (Fragment).
GN RPL16.
OS Gossypium darwinii (Darwin's cotton).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
OC eucotyledons; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=34276;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronin R.C., Seelman T., Wendel J.F.;
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group. ;
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031456; AAC63550.1; -;
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 958 MM; 71BSB/3411B40327 CRC64;
Query Match 100.0%; Score 15; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RTR 3
Db 3 RTR 5
RESULT 2
019958

ID 019958 PRELIMINARY; PRT; 8 AA.
 AC 019958;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Ribosomal protein L16 (Fragment).
 GN RPL16.
 OS Gossypium barbadense (Sea-island cotton) (Egyptian cotton).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvaceae; Gossypium.
 OX NCBI_TaxID=3634;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
 RT "The tortoise and the hare: choosing between noncoding plastome and
 RT nuclear Adh sequences for phylogeny reconstruction in a recently
 RT diverged plant group."
 RL Am. J. Bot. 85:1301-1315(1998).
 DR EMBL; AF031453; AAC63547.1; -;
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA: 958 MW: 71B5B73411B40327 CRC64;

Query Match 100.0%; Score 15; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
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 DB 3 RTR 5

RESULT 3
 ID 019960 PRELIMINARY; PRT; 8 AA.
 AC 019960;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Ribosomal protein L16 (Fragment).
 GN RPL16.
 OS Gossypium mustelinum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvaceae; Gossypium.
 OX NCBI_TaxID=34275;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
 RT "The tortoise and the hare: choosing between noncoding plastome and
 RT nuclear Adh sequences for phylogeny reconstruction in a recently
 RT diverged plant group."
 RL Am. J. Bot. 85:1301-1315(1998).
 DR EMBL; AF031455; AAC63549.1; -;
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA: 958 MW: 71B5B73411B40327 CRC64;

Query Match 100.0%; Score 15; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 |||
 DB 3 RTR 5

RESULT 4

ID 019959 PRELIMINARY; PRT; 8 AA.
 AC 019959;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Ribosomal protein L16 (Fragment).
 GN RPL16.
 OS Gossypium tomentosum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvaceae; Gossypium.
 OX NCBI_TaxID=34277;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
 RT "The tortoise and the hare: choosing between noncoding plastome and
 RT nuclear Adh sequences for phylogeny reconstruction in a recently
 RT diverged plant group."
 RL Am. J. Bot. 85:1301-1315(1998).
 DR EMBL; AF031454; AAC63548.1; -;
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA: 958 MW: 71B5B73411B40327 CRC64;

Query Match 100.0%; Score 15; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 |||
 DB 3 RTR 5

RESULT 5
 ID 019956 PRELIMINARY; PRT; 8 AA.
 AC 019956;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Ribosomal protein L16 (Fragment).
 GN RPL16.
 OS Gossypium arboreum (Tree cotton).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvaceae; Gossypium.
 OX NCBI_TaxID=29729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
 RT "The tortoise and the hare: choosing between noncoding plastome and
 RT nuclear Adh sequences for phylogeny reconstruction in a recently
 RT diverged plant group."
 RL Am. J. Bot. 85:1301-1315(1998).
 DR EMBL; AF031451; AAC63545.1; -;
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA: 958 MW: 71B5B73411B40327 CRC64;

Query Match 100.0%; Score 15; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 |||
 DB 3 RTR 5

RESULT 6

Q8MEM3 PRELIMINARY; PRT; 9 AA.
 AC Q8MEM3;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Howittia trilobularis.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eucosids II; Malvales; Malvaceae; Malvoideae; Howittia.
 OX NCBI_TaxID=183272;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhf and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL: AF384615; AAM50387.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA: 1256 MW: 6351D32409D411B4 CRC64;

Query Match 100.0%; Score 15; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
 III
 DB 2 RTR 4

RESULT 7

Q87617 PRELIMINARY; PRT; 10 AA.
 AC Q87617;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Tat protein (Fragment).
 GN TAT.
 OS Chimpazee immunodeficiency virus (SIV/cpz) (CIV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-G024;
 RX MEDLINE=97138325; Pubmed=8985351;
 RA Bibollet-Ruche F., Brengues C., Galat-Luong A., Galat G., Pourrut X.,
 RA Vidal N., Veas F., Durand J.P., Cuny G.;
 RT "Genetic diversity of simian immunodeficiency viruses from West
 RT African green monkeys: evidence of multiple genotypes within
 RT populations from the same geographical locale."
 RL J. Virol. 71:307-313(1997).
 DR EMBL: U37215; AAC56173.1; -.
 KW NON_TER 1 1
 FT NON_TER 10 AA: 1148 MW: 832608A2D411B411 CRC64;
 SQ SEQUENCE 10 AA: 1148 MW: 832608A2D411B411 CRC64;

Query Match 100.0%; Score 15; DB 15; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
 III
 DB 4 RTR 6

RESULT 8

Q8MEM7 PRELIMINARY; PRT; 11 AA.
 AC Q8MEM7;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Sida hookeriana.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eucosids II; Malvales; Malvaceae; Malvoideae; Sida.
 OX NCBI_TaxID=108446;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhf and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL: AF384624; AAM50396.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1470 MW: 7227C351D32409D4 CRC64;

Query Match 100.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
 III
 DB 2 RTR 4

RESULT 9

Q8MEM2 PRELIMINARY; PRT; 11 AA.
 AC Q8MEM2;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Lagunaria patersonia.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eucosids II; Malvales; Malvaceae; Malvoideae; Lagunaria.
 OX NCBI_TaxID=183274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhf and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL: AF384616; AAM50388.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1470 MW: 7227C351D32409D4 CRC64;

Query Match 100.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
 III
 DB 2 RTR 4

RESULT 10

Q8MEM5 PRELIMINARY; PRT; 11 AA.
 AC Q8MEM5;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Sida hookeriana.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eucosids II; Malvales; Malvaceae; Malvoideae; Sida.
 OX NCBI_TaxID=108446;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhf and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL: AF384624; AAM50396.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1470 MW: 7227C351D32409D4 CRC64;

AC 08MES1; 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN Rpl16.
 OS Abelsonschus manihoti.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Abelsonschus.
 OX NCBI_TaxID=183220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT *Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.*;
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384561; AAM50399.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SO SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 100.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 III
 DB 2 RTR 4

RESULT 11

ID 08MEP0; PRELIMINARY; PRT; 11 AA.
 AC 08MEP0;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN Rpl16.
 OS Hibiscus petalus.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183256;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT *Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.*;
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384598; AAM50370.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SO SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 100.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 III
 DB 2 RTR 4

RESULT 12

ID 08MER8; PRELIMINARY; PRT; 11 AA.
 AC 08MER8;

DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN Rpl16.
 OS Dombeya tiliacea.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Dombeyoideae; Dombeya.
 OX NCBI_TaxID=121875;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT *Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.*;
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384569; AAM50407.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SO SEQUENCE 11 AA; 1424 MW; 7227C351D32AE9D4 CRC64;

Query Match 100.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 III
 DB 2 RTR 4

RESULT 13

ID 08MES1; PRELIMINARY; PRT; 11 AA.
 AC 08MES1;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN Rpl16.
 OS Alyogyne plincolana.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.
 OX NCBI_TaxID=183226;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT *Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.*;
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384566; AAM50404.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SO SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 100.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 III
 DB 2 RTR 4

RESULT 14

ID 08MEP3; PRELIMINARY; PRT; 11 AA.
 AC 08MEP3;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus normanii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT *Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.*;
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL: AF384595; AAM50367.1; -
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 100.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 III
 DB 2 RTR 4

RESULT 15
 ID 08ME07 PRELIMINARY; PRT; 11 AA.
 AC 08ME07;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus drummondii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT *Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.*;
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL: AF384581; AAM50353.1; -
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 100.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTR 3
 III
 DB 2 RTR 4

Search completed: September 9, 2003, 23:34:24
 Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2003, 23:20:43 ; Search time 75 Seconds

(Without alignments)
10.582 Million cell updates/sec

Title: US-09-967-003-3

Perfect score: 27

Sequence: 1 RTRCG 5

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
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9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
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11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
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14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	21	AA21218
2	27	100.0	7	21	AA21221
3	27	100.0	8	21	AA21219
4	27	100.0	8	21	AA21222
5	27	100.0	10	22	AA21237
6	27	100.0	10	22	AA21239
7	27	100.0	32	22	AA21239
8	27	100.0	41	22	AA21239
9	27	100.0	50	22	AA21239

10	27	100.0	50	22	AA21239	Protonibacterium
11	27	100.0	52	23	ABP0475	Human ORF protein
12	27	100.0	55	23	ABP0684	Phaseolin promoter
13	27	100.0	55	23	ABP0689	Phaseolin promoter
14	27	100.0	59	18	AA21239	Soybean alpha-D-ga
15	27	100.0	60	23	ABP0754	Human secretory Po
16	27	100.0	61	22	AA212071	Protonibacterium
17	27	100.0	63	22	AA212071	Protonibacterium
18	27	100.0	64	23	ABP02149	Protonibacterium
19	27	100.0	70	22	AA21219	Protonibacterium
20	27	100.0	70	22	AA21219	Protonibacterium
21	27	100.0	80	22	AA21219	Protonibacterium
22	27	100.0	85	22	AA21219	Protonibacterium
23	27	100.0	92	22	AA21219	Protonibacterium
24	27	100.0	98	24	ABP09312	Human immune/haema
25	27	100.0	116	24	ABP09312	Human immune/haema
26	27	100.0	116	23	ABP07141	Human ORF ORP272
27	27	100.0	117	22	AA21219	Human ORF ORP272
28	27	100.0	125	19	AA21219	Human ORF ORP272
29	27	100.0	136	22	AA21219	Human ORF ORP272
30	27	100.0	140	21	AA21219	Human ORF ORP272
31	27	100.0	140	22	ABG05293	Human polypeptide
32	27	100.0	146	22	ABG05293	Human polypeptide
33	27	100.0	154	17	AA21219	Human polypeptide
34	27	100.0	159	21	AA21219	Human polypeptide
35	27	100.0	159	21	AA21219	Human polypeptide
36	27	100.0	159	21	AA21219	Human polypeptide
37	27	100.0	162	22	AA21219	Human polypeptide
38	27	100.0	169	21	AA21219	Human polypeptide
39	27	100.0	169	23	ABP0682	Human polypeptide
40	27	100.0	172	14	AA21219	Human polypeptide
41	27	100.0	173	14	AA21219	Human polypeptide
42	27	100.0	173	19	AA21219	Human polypeptide
43	27	100.0	173	19	AA21219	Human polypeptide
44	27	100.0	173	23	ABG32501	Human polypeptide
45	27	100.0	183	22	AA21219	Human polypeptide

ALIGNMENTS

RESULT 1	AA21218	standard; peptide; 5 AA.
ID	AA21218	
XX	AA21218	
AC	AA21218	
XX	AA21218	
DF	23-FEB-2001	(first entry)
XX	23-FEB-2001	
DE	Synthetic complementary peptide.	
XX	Synthetic complementary peptide.	
KM	Polymorphonuclear leukocyte; PMN; ophthalmological; anti-inflammatory;	
KM	PMN chemottractant antagonist; N-acetyl-PGP; N-acetyl-PGX; N-methyl-PGP;	
KM	neutrophil inhibitor; eye disease; alkali-injured eye;	
KM	chemically injured eye; inflammatory eye disease.	
XX	Synthetic.	
OS	Synthetic.	
XX	Synthetic.	
FT	Key	Location/Qualifiers
FT	Modified-site	5 /note="C-terminal amide"
XX	Modified-site	
PN	MO200053621-A2.	
XX	MO200053621-A2.	
PD	14-SEP-2000.	
XX	14-SEP-2000.	
XX	08-MAR-2000; 2000MO-US06062.	
PF	08-MAR-2000; 2000MO-US06062.	
XX	08-MAR-2000; 2000MO-US06062.	
PR	09-MAR-1999; 99US-0123409.	
XX	09-MAR-1999; 99US-0123409.	
PA	(HADD/) HADDX J L.	
PA	(BLAL/) BLALOCK J E.	
PA	(PFIS/) PFISTER R R.	

XX	(VILL/) VILLAIN M.
PI	Haddock JL, Bialock JE, Pfister RR, Villain M;
DR	WPI; 2000-611433/58.
XX	
XX	Pharmaceutical composition for treating eye diseases, comprises a
PT	peptide having sequence complementary to a specified sequence -
XX	
PS	Claim 3; Page 36; 42pp: English.
XX	
CC	The present sequence is a synthetic complementary peptide which is an
CC	antagonist of the polymorphonuclear leukocyte (PMN) chemottractant,
CC	N-acetyl-PGP. It is therefore useful for inhibiting PMN polarisation,
CC	chemotaxis and infiltration into tissue activated by neutrophil
CC	chemottractant such as N-acetyl-PGP, N-acetyl-PGX, N-methyl-PGP, or
CC	small peptide chemottractants containing proline and glycine. It may
CC	be used for treating eye diseases for e.g. alkali-injured eye,
CC	chemically injured eye and inflammatory eye disease. The present
CC	sequence is used as a monomer.
XX	
SO	Sequence 5 AA;
XX	
Query Match	100.0%; Score 27; DB 21; Length 5;
Best Local Similarity	100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 RTRGC 5
Db	1 RTRGC 5
XX	
RESULT 2	
ID	AAB21221
AC	AAB21221 standard; peptide; 7 AA.
XX	
AC	AAB21221;
XX	
DT	23-FEB-2001 (first entry)
XX	
DE	RTR dimer.
XX	
KM	PMN polymorphonuclear leukocyte; PMN; ophthalmological; antiinflammatory;
KM	PMN chemottractant antagonist; N-acetyl-PGP; N-acetyl-PGX; N-methyl-PGP;
KM	neutrophil inhibitor; eye disease; alkali-injured eye;
KM	chemically injured eye; inflammatory eye disease; RTR dimer.
XX	
OS	Synthetic.
XX	
XX	Key
FX	Location/Qualifiers
FT	1..5
FT	/note= "synthetic complementary peptide RTRGC"
FT	6
FT	/note= "Lys is linked to one copy of the RTRGC
FT	peptide through the alpha amino group; and to a
FT	second copy of the peptide (not shown) via the omega
FT	amino group.
XX	
XX	MO200053621-R2.
XX	
XX	14-SEP-2000.
XX	
XX	08-MAR-2000; 2000MO-US06062.
XX	
XX	09-MAR-1999; 99US-0123409.
XX	
XX	(HADD/) HADDOX J L.
PA	(BLAD/) BLADDOX J E.
PA	(PFIS/) PFISTER R R.
PA	(VILL/) VILLAIN M.
XX	
XX	Haddock JL, Bialock JE, Pfister RR, Villain M;

DR	WPI; 2000-611433/58.
PT	Pharmaceutical composition for treating eye diseases; comprises a
PT	peptide having sequence complementary to a specified sequence -
PS	Claim 3; Fig 1; 42pp: English.
CC	The present sequence is a synthetic complementary dimeric peptide
CC	which is an antagonist of the polymorphonuclear leukocyte (PMN)
CC	chemottractant, N-acetyl-PGP. It is useful for inhibiting PMN
CC	polarisation, chemotaxis and infiltration into tissue activated by
CC	neutrophil chemottractant such as N-acetyl-PGP, N-acetyl-PGX,
CC	N-methyl-PGP, or small peptide chemottractants containing proline
CC	and glycine. It may be used for treating eye diseases for
CC	e.g. alkali-injured eye, chemically injured eye and inflammatory
CC	eye disease.
XQ	Sequence 7 AA:
Query Match	100.0%; Score 27; DB 21; Length 7;
Best local Similarity	100.0%; Pred. No.9.3e+05;
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
Dy	1 RTRGG 5
	1 RTRGG 5
RESULT 3	
ID	AAB21219
	AAB21219 standard; peptide: 8 AA.
AC	AAB21219;
XX	
DT	23-FEB-2001 (first entry)
DE	RTR tetramer.
XX	
KM	Polymorphonuclear leukocyte; PMN; ophthalmological; antiinflammatory;
KW	PMN chemottractant antagonist; N-acetyl-PGP; N-acetyl-PGX; N-methyl-PGP;
KW	neutrophil inhibitor; eye disease; alkali-injured eye;
XX	chemically injured eye; inflammatory eye disease; RTR tetramer.
OS	Synthetic.
XX	
FH	Key
PH	Location/Qualifiers
FT	Peptide
FT	1..5
FT	/note= "synthetic complementary peptide RTRGG"
FT	Modified-site
FT	6
FT	/note= "Lys(6) is linked to one copy of the RTRGG
FT	peptide through the alpha amino group; and to a
FT	second copy of the peptide (not shown) via the omega
FT	amino group"
FT	7
FT	/note= "the alpha amino group of Lys (7) forms a
FT	peptide linkage with the carboxyl group of Lys(6);
FT	the omega amino group of Lys(7) forms a peptide bond
FT	with a second Lys residue analogous to Lys(6)"
PX	WO2000053621-A2.
PD	14-SEP-2000.
PF	08-MAR-2000; 2000MO-US06062.
PR	09-MAR-1999; 99US-0123409.
PA	(HADD/) HADDOX J L.
PA	(BLA/) BLALOCK J E.
PA	(PFI/) PFISTER R R.
PA	(VILL/) VILLAIN M.
Haddox JL, Blalock JE, Pfister RR, Villain M.	

XX DR WPI; 2000-611433/58.
 XX PT Pharmaceutical composition for treating eye diseases, comprises a
 XX peptide having sequence complementary to a specified sequence -
 XX PS Claim 3; Fig 1; 42pp; English.
 XX CC The present sequence is a synthetic complementary tetrameric peptide
 XX CC which is an antagonist of the polymorphonuclear leukocyte (PMN)
 XX CC chemoattractant, N-acetyl-PGP. It is useful for inhibiting
 XX CC PMN polarization, chemotaxis and infiltration into tissue activated
 XX CC by neutrophil chemoattractant such as N-acetyl-PGP, N-acetyl-PGX,
 XX CC N-methyl-PGP, or small peptide chemoattractants containing proline
 XX CC and glycine. It may be used for treating eye diseases for
 XX CC e.g. alkali-injured eye, chemically injured eye and inflammatory eye
 XX CC disease.
 XX SQ Sequence 8 AA:
 OY Query Match 100.0%; Score 27; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 RTRGG: 5
 11111
 1 RTRGG 5
 DB
 RESULT 4
 ID AAB21222 standard; peptide; 8 AA.
 AC AAB21222;
 DT 23-FEB-2001 (first entry)
 DE RFR tetramer containing dextrorotatory RFR sequences.
 XX PMN polymorphonuclear leukocyte; PMN: ophthalmological; anti-inflammatory;
 XX PMN chemoattractant antagonist; N-acetyl-PGP; N-acetyl-PGX; N-methyl-PGP;
 XX neutrophil inhibitor; eye disease; alkali-injured eye;
 XX chemically injured eye; inflammatory eye disease; RFR tetramer.
 OS Synthetic.
 XX Key Location/Qualifiers
 XX Peptide 1..5
 FT /note= "synthetic complementary peptide RTRGG"
 FT MISC-difference 1
 FT /note= "D-form residue"
 FT MISC-difference 2
 FT /note= "D-form residue"
 FT MISC-difference 3
 FT /note= "D-form residue"
 FT Modified-site 6
 FT /note= "Lys(6) is linked to one copy of the RTRGG
 FT peptide through the alpha amino group; and to a
 FT second copy of the peptide (not shown) via the omega
 FT amino group"
 FT Modified-site 7
 FT /note= "the alpha amino group of Lys (7) forms a
 FT peptide linkage with the carboxyl group of Lys(6);
 FT the omega amino group of Lys(7) forms a peptide bond
 FT with a second Lys residue analogous to Lys(6)"
 FT Modified-site 8
 FT /note= "C-terminal amide"
 XX PN WO200053621-A2.
 XX PD 14-SEP-2000.
 XX PF 08-MAR-2000; 2000WO-US06062.

XX PR 09-MAR-1999; 99US-0123409.
 XX PA (HADD/) HADDOX J L.
 XX PA (BLA/) BLALOCK J E.
 XX PA (PEIS/) PFISTER R R.
 XX PA (VILL/) VILLAIN M.
 XX PI Haddox JL, Blalock JE, Pfister RR, Villain M;
 XX DR WPI; 2000-611433/58.
 XX PT Pharmaceutical composition for treating eye diseases, comprises a
 XX PT peptide having sequence complementary to a specified sequence -
 XX PS Claim 3; Page 23; 42pp; English.
 XX CC The present sequence is a synthetic complementary tetrameric peptide
 XX CC which is an antagonist of the polymorphonuclear leukocyte (PMN)
 XX CC chemoattractant, N-acetyl-PGP. It is therefore useful for inhibiting
 XX CC PMN polarization, chemotaxis and infiltration into tissue activated by
 XX CC neutrophil chemoattractant such as N-acetyl-PGP, N-acetyl-PGX,
 XX CC N-methyl-PGP, or small peptide chemoattractants containing proline and
 XX CC glycine. It may be used for treating eye diseases for e.g. alkali-injured
 XX CC eye, chemically injured eye and inflammatory eye disease.
 XX SQ Sequence 8 AA:
 OY Query Match 100.0%; Score 27; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 RTRGG: 5
 11111
 1 RTRGG 5
 DB
 RESULT 5
 ID AAG87237 standard; peptide; 10 AA.
 AC AAG87237;
 DT 11-SEP-2001 (first entry)
 DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2186.
 XX DE
 XX Saccharomyces cerevisiae; complementary peptide; peptide identification;
 XX drug discovery; drug design.
 XX OS Saccharomyces cerevisiae.
 XX PN WO200142276-A1.
 XX PD 14-JUN-2001.
 XX PF 13-DEC-2000; 2000WO-GB04773.
 XX PR 13-DEC-1999; 99GB-0029471.
 XX PA (PROT-) PROTEOM LTD.
 XX PI Roberts GW, Heal JR;
 XX DR WPI; 2001-367863/38.
 XX PT Identifying complementary peptides by analysis of protein and
 XX PT nucleotide sequence databases, useful in drug design -
 XX PS Example 3; Page 331; 488pp; English.
 XX CC The invention relates to the identification of complementary peptides
 XX CC by analysis of protein and nucleotide sequence databases from higher

CC eukaryotic genomes, excluding human and plants. The specific
 CC complementary peptides interact with their relevant target proteins
 CC encoded in the eukaryotic genome. The peptides may be used as reagents
 CC and drugs for drug discovery and as lead ligands for drug design and
 CC development. The present sequence is a complementary peptide from
 CC Saccharomyces cerevisiae.

SO Sequence 10 AA:

Query Match

Best Local Similarity 100.0%; Score 27; DB 22; Length 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5

DB 4 RTRGC 8

RESULT 6

AA687239 standard; Peptide; 10 AA.

AC AAG87239;

DT 11-SEP-2001 (first entry)

DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2188.

KM Saccharomyces cerevisiae; complementary peptide; peptide identification;

XX drug discovery; drug design.

XX Saccharomyces cerevisiae.

PN WO200142276-A1.

PD 14-JUN-2001.

PF 13-DEC-2000; 2000MO-G804773.

PR 13-DEC-1999; 99GB-0029471.

PA (PROT-) PROTEOM LTD.

PI Roberts GW, Heal JR;

DR WPI; 2001-367863/38.

XX identifying complementary peptides by analysis of protein and

PT nucleotide sequence databases, useful in drug design -

XX Example 3; Page 331; 488pp; English.

CC The invention relates to the identification of complementary peptides

CC by analysis of protein and nucleotide sequence databases from higher

CC eukaryotic genomes, excluding human and plants. The specific

CC complementary peptides interact with their relevant target proteins

CC encoded in the eukaryotic genome. The peptides may be used as reagents

CC and drugs for drug discovery and as lead ligands for drug design and

CC development. The present sequence is a complementary peptide from

CC Saccharomyces cerevisiae.

SO Sequence 10 AA:

Query Match

Best Local Similarity 100.0%; Score 27; DB 22; Length 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7

AA676092
 ID AA676092 standard; Protein; 32 AA.
 XX
 AC AA676092;
 XX
 DT 03-SEP-2001 (first entry)
 DE Human colon cancer antigen protein SEQ ID NO:6856.
 XX
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KM colorectal carcinoma; chromosome 10.
 KW
 XX Homo sapiens.
 OS
 PN WO200122920-A2.
 PD 05-APR-2001.
 PF 28-SEP-2000; 2000MO-US26524.
 PR 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 XX
 PA (HDMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 DR WPI; 2001-235357/24.
 DR N-PSDB; AAH35497.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 PS Claim 11; Page 8303; 9803pp; English.
 XX
 XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated P,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAB7789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 606 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SO Sequence 32 AA:
 Query Match
 Best Local Similarity 100.0%; Score 27; DB 22; Length 32;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RTRGC 5
 DB 26 RTRGC 30
 RESULT 8
 AA682229
 ID AA682229 standard; Protein; 41 AA.
 XX
 AC AA682229;
 XX
 DT 07-NOV-2001 (first entry)

XX DE Human immune/haematopoietic antigen SEQ ID NO:9822.
XX XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW Cytostatic; gene therapy; vaccine; metastasis.
OS Homo sapiens.
XX WO200157182-A2.
XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01354.
XX XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220966.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226581.
PR 22-AUG-2000; 2000US-0226586.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229347.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0233397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.

PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 03-DEC-2000; 2000US-0250391.
PR 03-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.

PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-483426/52.
 DR N-PSDB; AAK55010.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 PS
 PS Claim 11; SEQ ID NO 9822; 3071bp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM62170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent
 CC disease and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK67694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM62169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 41 AA;
 QY 1 RTRGG 5
 Db 19 RTRGG 23
 Query Match 100.0%; Score 27; DB 22; Length 41;
 Best Local Similarity 100.0%; Pred. No. 1,4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
 AA059446
 ID AA059446 standard; Protein: 50 AA.
 XX
 AC AA059446;
 XX
 DT 27-FEB-2002 (first entry)
 DE
 XX
 DE Propionibacterium acnes immunogenic protein #20342.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 PD
 XX
 PD 01-NOV-2001.
 PF
 XX
 PF 20-APR-2001; 2001WO-US12865.
 PR
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.

XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skelky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'Maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59602.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 PS
 PS Example 1; SEQ ID NO 20641; 1069bp; English.
 XX
 CC Sequences AA039105-AA068017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 50 AA;
 QY 1 RTRGG 5
 Db 26 RTRGG 30
 Query Match 100.0%; Score 27; DB 22; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
 AA067751
 ID AA067751 standard; Protein: 50 AA.
 XX
 AC AA067751;
 XX
 DT 27-FEB-2002 (first entry)
 DE
 XX
 DE Propionibacterium acnes immunogenic protein #28647.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 PD
 XX
 PD 01-NOV-2001.
 PF
 XX
 PF 20-APR-2001; 2001WO-US12865.
 PR
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.

XX	30-MAY-2000:	2000US-206133P.
PR	29-AUG-2000:	2000US-228716P.
XX	(CURA-) CUREGEN CORP.	
PA		
XX	Shimkets RA, Leach MD:	
DR	WPI: 2002-106308/14.	
XX	N-PSDB: ABN16227.	
XX		
PT	Novel human polypeptides and polynucleotides useful for diagnosing,	
PT	preventing and treating cardiovascular disease, neurodegenerative,	
PT	hyperproliferative disorders and autoimmune disorders	
PS	Disclosure: SEQ ID 932; 1037p; English.	
XX		
CC	The present invention describes substantially purified human proteins	
CC	(referred to as open reading frame, ORFX, where x is 1-11491 (see Table 1	
CC	In the specification)). ABN15762 to ABN27252 encode the human ORFX	
CC	proteins given in ABP000010 to ABP11500. ORFX proteins are useful for	
CC	treating or preventing a pathology associated with an ORFX-associated	
CC	disorder in humans, and in the manufacture of a medicament for treating a	
CC	syndrome associated with ORFX-associated disorder. ORFX polynucleotide	
CC	sequences can be used in gene therapy. ORFX sequences can be used in the	
CC	treatment of cancer, hyperproliferative disorders, cirrhosis of liver,	
CC	psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,	
CC	osteoarthritis, neurodegenerative disorders, disorders related to organ	
CC	transplantation, cardiovascular diseases, diabetes mellitus, systemic	
CC	lupus erythematosus, hypertension, hypothyroidism, cholesterol ester	
CC	storage disease, various immune deficiencies and disorders, infectious	
CC	diseases, autoimmune disorders such as multiple sclerosis, rheumatoid	
CC	arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host	
CC	disease and autoimmune inflammatory eye disease. ORFX proteins are also	
CC	useful for treating burns, incisions, ulcers, for treating osteoporosis,	
CC	bone degenerative disorders, or periodontal disease, and for gut	
CC	protection or regeneration and treatment of lung or liver fibrosis,	
CC	repertusion injury in various tissues and conditions resulting from	
CC	systemic cytokine damage.	
CC	N.B. The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences.	
XX		
XX	Sequence 52 AA:	
SO		
XX		
XX	Query Match	100.0% Score 27; DB 23; Length 52;
XX	Best Local Similarity	100.0%; Pred. No. 1,7e+02;
XX	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 RTGGG 5	
XX		
Db	5 RTGGG 9	
XX		
XX	RESULT 12	
XX	ABP60684	
ID	ABP60684 standard; Protein: 55 AA.	
AC	ABP60684:	
XX		
XX	06-SEP-2002 (first entry)	
DE	Phaseolin promoter-Trxh oleosin-phaseolin terminator SEQ:21.	
XX		
KM	Multimeric protein; redox protein; thiorodoxin; thiorodoxin reductase;	
KM	oil body; ophthalmological; antidiabetic; cytosolic; antipsoriatic;	
KM	vasotropic; vulnary; antibacterial; immunosuppressive; anticancer;	
KM	food product; milk; wheat; oxidative stress; catarract; diabetes;	
KM	chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;	
KM	bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;	
KM	gastro intestinal bleeding; intestinal bowel disease; ulcer;	
KM	gastro oesophageal reflux disease.	
XX		

OS Arabidopsis sp.
OS Phaseolus vulgaris.
XX WO200250289-A1.
XX
XX 27-JUN-2002.
PD
XX 19-DEC-2001; 2001MO-US50240.
XX
XX 19-DEC-2000; 2000US-0742900.
PR 05-JUL-2001; 2001US-302885P.
PR 04-DEC-2001; 2001US-0006038.
XX
PA (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
PI Del Val G, Zaplachinski S, Moloney M;
XX WPI; 2002-508806/54.
DR N-PSDB; ABN89581.
XX
XX Producing oil body associated with recombinant multimeric protein
PT complex e.g. redox proteins and immunoglobulins comprises producing
PT recombinant polypeptides capable of forming the complex in cells
PT comprising oil bodies -
XX
XX
PS Disclosure; Page 172; 362pp; English.
XX
XX The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating
CC with P2 to form the MPC and associating the complex with an occluding
CC body (OB) through an OB-targeting-protein capable of associating with OB
CC and P1. M1 is useful for producing an oil body associated with a
CC recombinant MPC. The oil bodies are further formulated for use in the
CC preparation of a food product such as milk or wheat based food product,
CC personal care product which reduces the oxidative stress on the surface
CC area of the human body or used to lighten the skin, or a pharmaceutical
CC composition used to treat chronic obstructive pulmonary disease (COPD),
CC cataracts, diabetes, envenomation, bronchiolopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677
CC to ABP60964 represent sequence given in the exemplification of the
CC present invention.
XX
XX Sequence 55 AA:
SQ
Query Match 100.0%; Score 27; DB 23; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RTRGG 5
DB 47 RTRGG 51
RESULT 13
ID ABP60689
XX ABP60689; standard; Protein; 55 AA.
AC
XX ABP60689;
XX
XX 06-SEP-2002 (first entry)
DE Phaseolin promoter-thioredoxin reductase oleosin-terminator SEQ.29.
XX
XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
KM oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
KM vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
KM food product; milk; wheat; oxidative stress; cataract; diabetes.

KM Chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KM bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing;
KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
KM gastro oesophageal reflux disease.
XX
XX Arabidopsis sp.
OS Phaseolus vulgaris.
XX WO200250289-A1.
XX
XX 27-JUN-2002.
PD
XX 19-DEC-2001; 2001MO-US50240.
XX
XX 19-DEC-2000; 2000US-0742900.
PR 05-JUL-2001; 2001US-302885P.
PR 04-DEC-2001; 2001US-0006038.
XX
PA (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
PI Del Val G, Zaplachinski S, Moloney M;
XX WPI; 2002-508806/54.
DR N-PSDB; ABN89584.
XX
XX Producing oil body associated with recombinant multimeric protein
PT complex e.g. redox proteins and immunoglobulins comprises producing
PT recombinant polypeptides capable of forming the complex in cells
PT comprising oil bodies -
XX
XX
PS Disclosure; Page 184; 362pp; English.
XX
XX The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating
CC with P2 to form the MPC and associating the complex with an occluding
CC body (OB) through an OB-targeting-protein capable of associating with OB
CC and P1. M1 is useful for producing an oil body associated with a
CC recombinant MPC. The oil bodies are further formulated for use in the
CC preparation of a food product such as milk or wheat based food product,
CC personal care product which reduces the oxidative stress on the surface
CC area of the human body or used to lighten the skin, or a pharmaceutical
CC composition used to treat chronic obstructive pulmonary disease (COPD),
CC cataracts, diabetes, envenomation, bronchiolopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677
CC to ABP60964 represent sequence given in the exemplification of the
CC present invention.
XX
XX Sequence 55 AA:
SQ
Query Match 100.0%; Score 27; DB 23; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RTRGG 5
DB 47 RTRGG 51
RESULT 14
ID AAM10323
XX AAM10323 standard; Peptide; 59 AA.
AC
XX AAM10323;
XX
XX 03-MAY-1997 (first entry)
DE Soybean alpha-D-galactosidase signal peptide.

```

XX Alpha-D-galactosidase; soybean; deantigenation enzyme;
KW blood type O; antigen; seroconversion; blood transfusion;
KW erythrocyte.
XX
XX Glycine max.
XX W09640714-A1.
XX
XX 19-DEC-1996.
XX
XX 08-MAY-1996; 96MO-US06511.
XX
XX 07-JUN-1995; 95US-0488961.
XX 08-SEP-1994; 94US-0303156.
XX
XX (UNOR ) UNIV MISSOURI.
XX
XX Smith DS, Walker JC;
XX WPI: 1997-052216/05.
XX N-PSDB; AAT47065.
XX
XX Recombinant alpha-D-galactosidase(s) from glycine and Phaseolus -
XX useful as deantigenation enzymes to convert type B erythrocytes to
XX type O cells for blood transfusion
XX
XX Example 6; Page 42; 61pp; English.
XX
XX A signal peptide (AAM10323) and mature alpha-D-galactosidase (AAM10320)
XX are encoded by a cDNA clone (AAT47065) isolated from a soybean cDNA
XX library. The mature enzyme can be used to convert type B
XX erythrocytes to type O cells for use in blood transfusions.
XX
XX Sequence 59 AA;
XX
XX Query Match 100.0%; Score 27; DB 18; Length 59;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RTRGG 5
DB 42 RTRGG 46

RESULT 15
ABB97754
ID ABB97754 standard; Protein; 60 AA.
XX
XX ABB97754;
AC
XX
XX 03-OCT-2002 (first entry)
DT
XX
XX Human secretory polypeptide (SPTM) 6.
DE
XX
XX Human; secretory protein; secretory polynucleotides; SPTM;
KW SPTM-related disease; somatic gene therapy; germine gene therapy;
KW severe combined immunodeficiency; intracellular parasite protection;
KW fungal parasite; protozoan parasite; cell proliferative disorder; cancer;
KW immune disorder; AIDS; neurological disorder; Parkinson's disease;
KW motor neuron disorder; demyelinating disease; multiple sclerosis;
KW meningitis; abscess; prion diseases; cerebral palsy;
KW neuroskeletal disorder; peripheral nervous system disorder;
KW dermatomyositis; polymyositis; myopathy; myasthenia gravis;
KW mental disorder; Tourette's syndrome.
XX
XX Homo sapiens.
OS
XX
XX W0200220756-A2.
PN
XX
XX 14-MAR-2002.
PD
XX
XX 30-AUG-2001; 2001MO-US27297.
PF

```

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XX 05-SEP-2000; 2000US-229747P.
PR 05-SEP-2000; 2000US-229748P.
PR 05-SEP-2000; 2000US-229749P.
PR 05-SEP-2000; 2000US-229750P.
PR 05-SEP-2000; 2000US-229751P.
PR 05-SEP-2000; 2000US-230016P.
PR 05-SEP-2000; 2000US-230583P.
PR 05-SEP-2000; 2000US-230589P.
PR 05-SEP-2000; 2000US-230514P.
PR 05-SEP-2000; 2000US-230515P.
PR 05-SEP-2000; 2000US-230517P.
PR 05-SEP-2000; 2000US-230518P.
PR 05-SEP-2000; 2000US-230519P.
PR 05-SEP-2000; 2000US-230595P.
PR 05-SEP-2000; 2000US-230596P.
PR 05-SEP-2000; 2000US-230597P.
PR 05-SEP-2000; 2000US-230599P.
PR 05-SEP-2000; 2000US-230610P.
PR 05-SEP-2000; 2000US-230864P.
PR 05-SEP-2000; 2000US-230865P.
PR 05-SEP-2000; 2000US-230988P.
PR 05-SEP-2000; 2000US-230989P.
PR 05-SEP-2000; 2000US-230990P.
PR 05-SEP-2000; 2000US-230896P.
PR 05-SEP-2000; 2000US-230897P.
PR 05-SEP-2000; 2000US-230951P.
PR 05-SEP-2000; 2000US-231163P.
PR 05-SEP-2000; 2000US-231832P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Stuart J., Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
XX Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
XX Momiya MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
XX Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Datto A;
XX Marwaha R, Chen AJ, Chang SC, Au AP, Imman KR;
XX
XX WPI: 2002-315658/35.
XX N-PSDB; ABL9751.
XX
XX Polynucleotide sequences encoding human secretory proteins useful for
XX gene therapy of e.g. genetic deficiency disorders, cancers, and
XX diseases caused by intracellular parasites -
XX
XX Claim 29; Page 367; 585pp; English.
XX
XX The invention comprises the amino acid and coding sequences of human
XX secretory (SPTM) proteins. The SPTM DNA and amino acid sequences are
XX useful for treating a disease or condition associated with the expression
XX of functional SPTM. The SPTM DNA sequences are useful for somatic or
XX germine gene therapy to correct a genetic deficiency (e.g. severe
XX combined immunodeficiency). The SPTM DNA sequences are also useful in
XX providing protection against intracellular parasites (e.g. fungal
XX parasites and protozoan parasites). The SPTM DNA and protein sequences
XX are also useful for diagnosing cell proliferative disorders, cancer,
XX immune disorders (e.g. AIDS), neurological disorders (e.g. Parkinson's
XX disease), motor neuron disorders, demyelinating diseases (e.g. multiple
XX sclerosis), meningitis, abscesses, prion diseases, cerebral palsy,
XX neuroskeletal disorders, peripheral nervous system disorders,
XX dermatomyositis and polymyositis, myopathy, myasthenia gravis, and mental
XX disorders (e.g. Tourette's syndrome). Amino acid sequences ABB97749 -
XX ABB97933 represent human secretory proteins of the invention.
XX
XX Sequence 60 AA;
SO
XX
XX Query Match 100.0%; Score 27; DB 23; Length 60;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RTRGG 5
DB 40 RTRGG 44

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Search completed: September 9, 2003, 23:31:42
Job time : 77 secs

GenCore version 5.1.6
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OH protein - protein search, using sw model

Run on: September 9, 2003, 23:29:38 ; Search time 25.625 Seconds

(Without alignments)
8.256 Million cell updates/sec

Title: US-09-967-003-3

Perfect score: 27

Sequence: 1 RTRGG 5

Scoring table:

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Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents_AA.*

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3: /cgn2_6/ptodata/1/aa/5A.COMB.pep.*
4: /cgn2_6/ptodata/1/aa/5B.COMB.pep.*
5: /cgn2_6/ptodata/1/aa/PTCUTS.COMB.pep.*
6: /cgn2_6/ptodata/1/aa/Backfillseq1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	4	US-09-521-365A-3
2	27	100.0	55	2	US-08-846-021A-3
3	27	100.0	59	1	US-08-488-961-3
4	27	100.0	59	3	US-08-973-297-3
5	27	100.0	59	5	PCT-US96-06511-3
6	27	100.0	121	4	US-09-252-991A-19703
7	27	100.0	125	2	US-08-767-026-5
8	27	100.0	125	4	US-09-319-275A-5
9	27	100.0	129	4	US-09-732-210-1664
10	27	100.0	142	4	US-09-252-991A-21581
11	27	100.0	154	1	US-08-366-783-5
12	27	100.0	173	1	US-08-366-783-2
13	27	100.0	173	1	US-08-313-098A-2
14	27	100.0	173	2	US-08-767-026-2
15	27	100.0	173	2	US-08-831-575-6
16	27	100.0	173	4	US-09-319-275A-2
17	27	100.0	187	4	US-08-846-021A-5
18	27	100.0	191	4	US-09-252-991A-27186
19	27	100.0	195	4	US-09-252-991A-21779
20	27	100.0	234	1	US-08-366-783-4
21	27	100.0	254	2	US-08-767-026-7
22	27	100.0	264	4	US-09-319-275A-7
23	27	100.0	268	4	US-09-252-991A-26485
24	27	100.0	299	4	US-09-319-275A-2
25	27	100.0	299	4	US-10-090-190-2
26	27	100.0	305	4	US-09-252-991A-28580
27	27	100.0	307	4	US-09-252-991A-17085

28	27	100.0	314	4	US-09-252-991A-20396	Sequence 20396, A
29	27	100.0	321	4	US-09-996-243-36	Sequence 36, Appl
30	27	100.0	324	4	US-09-319-275A-14	Sequence 14, Appl
31	27	100.0	341	4	US-09-252-991A-20062	Sequence 20062, A
32	27	100.0	354	4	US-09-198-452A-504	Sequence 504, App
33	27	100.0	366	3	US-09-210-843-2	Sequence 2, Appl1
34	27	100.0	377	4	US-09-252-991A-24675	Sequence 24675, A
35	27	100.0	393	4	US-09-252-991A-25633	Sequence 25633, A
36	27	100.0	427	2	US-08-846-021A-8	Sequence 8, Appl1
37	27	100.0	532	1	US-08-594-447-1	Sequence 1, Appl1
38	27	100.0	532	2	US-08-665-647-1	Sequence 11, Appl1
39	27	100.0	537	4	US-08-426-509A-11	Sequence 11, Appl
40	27	100.0	537	4	US-08-232-545-11	Sequence 11, Appl
41	27	100.0	537	5	PCT-US95-05008-11	Sequence 11, Appl
42	27	100.0	546	4	US-09-252-991A-27606	Sequence 27606, A
43	27	100.0	630	4	US-09-252-991A-25626	Sequence 25626, A
44	27	100.0	803	4	US-09-252-991A-23614	Sequence 23614, A
45	27	100.0	869	4	US-09-252-991A-22290	Sequence 22290, A

ALIGNMENTS

RESULT 1
US-09-521-365A-3
Sequence 3, Application US/09521365A
Patent No. 6310041
GENERAL INFORMATION:
APPLICANT: Haddox, Jeffrey
APPLICANT: Pfister, Robert
APPLICANT: Blalock, James
APPLICANT: Matteo, Villain
TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC USES THEREOF
FILE REFERENCE: 92750/57
CURRENT APPLICATION NUMBER: US/09/521,365A
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: US 60/123,409
PRIORITY DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 5
TYPE: PRT
ORGANISM: artificial sequence
FEATURES:
OTHER INFORMATION: description of artificial sequence: amino acid
OTHER INFORMATION: sequence of complementary peptide inhibitor of
OTHER INFORMATION: neutrophils; used as a monomer
US-09-521-365A-3
Query Match
Best Local Similarity 100.0%; Score 27; DB 4; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OO 1 RTRGG 5
Db 1 RTRGG 5
US-08-846-021A-3
Sequence 3, Application US/08846021A
Patent No. 5946882
GENERAL INFORMATION:
APPLICANT: Moloney, Maurice M.
TITLE OF INVENTION: Preparation of Heterologous Proteins on
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario

COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,021A
FILING DATE: April 25, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 9369-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-021A-3

Query Match 100.0%; Score 27; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGG 5
DB 47 RTRGG 51

RESULT 3
US-08-488-961-3
Sequence 3, Application US/08488961
Patent No. 5606042
GENERAL INFORMATION:
APPLICANT: Smith, Daniel S.
APPLICANT: Walker, John C.
TITLE OF INVENTION: Glycine and Phaseolus
NUMBER OF INVENTION: alpha-D-Galactosidases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Echington, Barnard & Perry
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: US
ZIP: 48099-4390
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,961
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-320 (Umo)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 689-3500
TELEFAX: (810) 689-4071
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-488-961-3

Query Match 100.0%; Score 27; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGG 5
DB 42 RTRGG 46

RESULT 4
US-08-973-297-3
Sequence 3, Application US/08973297
Patent No. 6184017
GENERAL INFORMATION:
APPLICANT: Smith, Daniel S.
APPLICANT: Walker, John C.
TITLE OF INVENTION: Glycine and Phaseolus
NUMBER OF INVENTION: alpha-D-Galactosidases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 6184017thwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,297
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 0994,00050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-973-297-3

Query Match 100.0%; Score 27; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGG 5
DB 42 RTRGG 46

RESULT 5
PCT-US96-06511-3
Sequence 3, Application PC/TUS9606511
GENERAL INFORMATION:
APPLICANT: Smith, Daniel S.
APPLICANT: Walker, John C.
TITLE OF INVENTION: Glycine and Phaseolus
NUMBER OF INVENTION: alpha-D-Galactosidases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates

STREET: 30500 Northwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06511
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 0994,00050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US96-06511-3

Query Match
Best Local Similarity 100.0%; Score 27; DB 5; Length 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
|||||
DB 42 RTRGG 46

RESULT 6
US-09-252-991A-19703
Sequence 19703 Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19703
LENGTH: 121
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19703

Query Match
Best Local Similarity 100.0%; Score 27; DB 4; Length 121;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
|||||
DB 3 RTRGG 7

RESULT 7
US-08-767-026-5
Sequence 5, Application US/08767026
Patent No. 5856452

GENERAL INFORMATION:
APPLICANT: Moloney, Maurice
APPLICANT: Boothe, Joseph
APPLICANT: van Rooijen, GJ's
TITLE OF INVENTION: Oil Bodies and Associated Proteins as
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERSKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,026
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Michelle
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 3969-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-767-026-5

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 125;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
|||||
DB 47 RTRGG 51

RESULT 8
US-09-319-275A-5
Sequence 5, Application US/09319275A
Patent No. 6509453
GENERAL INFORMATION:
APPLICANT: Moloney, Maurice
APPLICANT: Boothe, Joseph
APPLICANT: Rooijen, GJ's Van
TITLE OF INVENTION: Oil Bodies and Associated Proteins as Affinity Matrices
FILE REFERENCE: 9369-85
CURRENT FILING DATE: 1999-08-27
CURRENT APPLICATION NUMBER: US/09/319,275A
PRIOR FILING DATE: 1997-12-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 125
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oleosin - Hirudin Fusion
US-09-319-275A-5

Query Match
Best Local Similarity 100.0%; Score 27; DB 4; Length 125;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
|||||
Db 47 RTRGC 51

RESULT 9

US-09-732-210-1664
; Sequence 1664, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yomle S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1664
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Methanococcus jannaschii
US-09-732-210-1664

Query Match

Best Local Similarity 100.0%; Score 27; DB 4; Length 129;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
|||||
Db 48 RTRGC 52

RESULT 10

US-09-252-991A-21581
; Sequence 21581, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Mate J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 3142
; SEQ ID NO 21581
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21581

Query Match

Best Local Similarity 100.0%; Score 27; DB 4; Length 142;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
|||||
Db 11 RTRGC 15

RESULT 11

US-08-366-783-5
; Sequence 5, Application US/08366783
; Patent No. 5650554
; GENERAL INFORMATION:
; APPLICANT: Moloney, Maurice M
; TITLE OF INVENTION: Oil-Body Proteins As Carriers of
; TITLE OF INVENTION: High-Value Peptides in Plants
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DEHLINGER & ASSOCIATES
; STREET: 350 CAMBRIDGE AVENUE, SUITE 250
; CITY: PALO ALTO
; STATE: California
; COUNTRY: United States
; ZIP: 94025-1536
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,783
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: FABIAN, GARY
; REGISTRATION NUMBER: 33,875
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-324-0880
; TELEFAX: 415-324-0960
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-366-783-5

Query Match

Best Local Similarity 100.0%; Score 27; DB 1; Length 154;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
|||||
Db 146 RTRGC 150

RESULT 12

US-08-366-783-2
; Sequence 2, Application US/08366783
; Patent No. 5650554
; GENERAL INFORMATION:
; APPLICANT: Moloney, Maurice M
; TITLE OF INVENTION: Oil-Body Proteins As Carriers of
; TITLE OF INVENTION: High-Value Peptides in Plants
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DEHLINGER & ASSOCIATES
; STREET: 350 CAMBRIDGE AVENUE, SUITE 250
; CITY: PALO ALTO
; STATE: California
; COUNTRY: United States
; ZIP: 94025-1536
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,783
; FILING DATE:
; CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: FABIAN, GARY
REGISTRATION NUMBER: 33,875
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: ARABIDOPSIS THALIANA
US-08-366-783-2

Query Match 100.0%; Score 27; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
11111
DB 165 RTRGC 169

RESULT 13
US-08-313-098A-2
Sequence 2, Application US/08313098A
Patent No. 5709922
GENERAL INFORMATION:
APPLICANT: Moloney, Maurice M.
TITLE OF INVENTION: OIL-BODY PROTEIN CIS-ELEMENTS AS
TITLE OF INVENTION: REGULATORY SIGNALS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEIL, GOTSCHAL & MANGES
STREET: 2882 SAND HILL ROAD, STE. 280
CITY: MENLO PARK
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,098A
FILING DATE: 27-JANUARY-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/659,835
FILING DATE: 22-FEBRUARY-1991
APPLICATION NUMBER: PCT/CA92/00161
FILING DATE: 15-APRIL-1992
APPLICATION NUMBER: US 07/862,355
FILING DATE: 02-APRIL-1992
APPLICATION NUMBER: PCT/CA93/00141
FILING DATE: 02-APRIL-1993
APPLICATION NUMBER: US 08/142,418
FILING DATE: 16-NOVEMBER-1993
APPLICATION NUMBER: US 08/196,772
FILING DATE: 15-FEBRUARY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Ventler, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: UNTE-010/0305
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 173 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-098A-2

Query Match 100.0%; Score 27; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
11111
DB 165 RTRGC 169

RESULT 14
US-08-767-026-2
Sequence 2, Application US/08767026
Patent No. 586452
GENERAL INFORMATION:
APPLICANT: Moloney, Maurice
APPLICANT: Boothe, Joseph
APPLICANT: van Rooijen, Gijb
TITLE OF INVENTION: Oil Bodies and Associated Proteins as
TITLE OF INVENTION: Affinity Matrices
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,026
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Michelle
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 9369-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-767-026-2

Query Match 100.0%; Score 27; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
11111
DB 165 RTRGC 169

RESULT 15
US-08-831-575-6
Sequence 6, Application US/08831575
Patent No. 5977436
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Li, Zhongsen

;; TITLE OF INVENTION: AN OLEOSIN 5' REGULATORY REGION FOR THE
;; TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION
;; NUMBER OF SEQUENCES: 33
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
;; STREET: 400 Garden City Plaza
;; CITY: Garden City
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 11530
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/831,575
;; FILING DATE: 09-APR-1997
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DIGILLO, Frank S.
;; REGISTRATION NUMBER: 31,346
;; REFERENCE/DOCKET NUMBER: 10203
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (516) 742-4343
;; TELEFAX: (516) 742-4366
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 173 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-831-575-6

Query Match 100.0%; Score 27; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTGCG 5
|||||
Db 165 RTGCG 169

Search completed: September 9, 2003, 23:36:08
Job time : 26.625 secs

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OM protein - protein search, using SW model

Run on: September 9, 2003, 23:34:34 ; Search time 46.875 Seconds

(without alignments)
14.646 Million cell updates/sec

Title: US-09-967-003-3

Perfect score: 27

Sequence: 1 RTRCG 5

Scoring table:

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Gapop 10.0, Gapext 0.5

Searched: 513375 seqs, 137303645 residues

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications, AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	10 US-09-967-003-3	Sequence 3, Appl1
2	27	100.0	32	15 US-10-106-698-6866	Sequence 6866, Ap
3	27	100.0	44	12 US-10-037-243-9	Sequence 9, Appl1
4	27	100.0	55	9 US-09-897-898-12	Sequence 12, Appl
5	27	100.0	55	9 US-09-897-898-20	Sequence 20, Appl
6	27	100.0	55	11 US-09-893-525-3	Sequence 3, Appl1
7	27	100.0	125	15 US-10-260-562-5	Sequence 5, Appl1
8	27	100.0	125	15 US-10-260-562-5	Sequence 5, Appl1
9	27	100.0	146	10 US-09-738-626-6573	Sequence 6573, Ap
10	27	100.0	162	10 US-09-747-155-173	Sequence 173, Ap
11	27	100.0	169	9 US-09-897-898-9	Sequence 9, Appl1
12	27	100.0	173	15 US-10-260-960-2	Sequence 2, Appl1
13	27	100.0	173	15 US-10-260-562-2	Sequence 2, Appl1
14	27	100.0	187	11 US-09-893-525-5	Sequence 5, Appl1
15	27	100.0	194	9 US-09-910-562-4	Sequence 4, Appl1

16	27	100.0	226	12 US-10-237-496-112	Sequence 112, App
17	27	100.0	226	12 US-10-242-074-112	Sequence 112, App
18	27	100.0	226	12 US-10-242-505-112	Sequence 112, App
19	27	100.0	226	12 US-10-242-574-112	Sequence 112, App
20	27	100.0	226	12 US-10-243-261-112	Sequence 112, App
21	27	100.0	226	12 US-10-243-282-112	Sequence 112, App
22	27	100.0	226	12 US-10-243-402-112	Sequence 112, App
23	27	100.0	226	12 US-10-243-431-112	Sequence 112, App
24	27	100.0	226	12 US-10-245-164-112	Sequence 112, App
25	27	100.0	226	15 US-10-245-103-112	Sequence 112, App
26	27	100.0	226	15 US-10-245-107-112	Sequence 112, App
27	27	100.0	226	15 US-10-245-143-112	Sequence 112, App
28	27	100.0	226	15 US-10-245-171-112	Sequence 112, App
29	27	100.0	226	15 US-10-245-751-112	Sequence 112, App
30	27	100.0	226	15 US-10-245-883-112	Sequence 112, App
31	27	100.0	226	15 US-10-237-535-112	Sequence 112, App
32	27	100.0	226	15 US-10-238-183-112	Sequence 112, App
33	27	100.0	226	15 US-10-238-283-112	Sequence 112, App
34	27	100.0	226	15 US-10-238-370-112	Sequence 112, App
35	27	100.0	226	15 US-10-245-055-112	Sequence 112, App
36	27	100.0	226	15 US-10-245-147-112	Sequence 112, App
37	27	100.0	226	15 US-10-245-730-112	Sequence 112, App
38	27	100.0	226	15 US-10-245-739-112	Sequence 112, App
39	27	100.0	226	15 US-10-246-210-112	Sequence 112, App
40	27	100.0	226	15 US-10-239-196-112	Sequence 112, App
41	27	100.0	226	15 US-10-243-024-112	Sequence 112, App
42	27	100.0	226	15 US-10-243-409-112	Sequence 112, App
43	27	100.0	226	15 US-10-245-621-112	Sequence 112, App
44	27	100.0	226	15 US-10-245-880-112	Sequence 112, App
45	27	100.0	226	15 US-10-245-033-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-09-967-003-3
Sequence 3, Application US/09967003
Patent No. US20020107202A1
GENERAL INFORMATION:
APPLICANT: Haddox, Jeffrey
APPLICANT: Pfister, Robert
APPLICANT: Blalock, James
TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC
FILE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/09/967,003
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/521,365
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: US 60/123,409
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 5
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: description of artificial sequence: amino acid
OTHER INFORMATION: sequence of complementary peptide inhibitor of
OTHER INFORMATION: neutrophils; used as a monomer
US-09-967-003-3

Query Match
Best Local Similarity 100.0%; Score 27; DB 10; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RTRCG 5
1 RTRCG 5
1 RTRCG 5
1 RTRCG 5

RESULT 2
US-10-106-698-6866
; Sequence 6866, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6866
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (117)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (22)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (23)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (25)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6866
Query Match 100.0%; Score 27; DB 15; Length 32;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RTRGG 5
DB 26 RTRGG 30
RESULT 3
US-10-037-243-9
; Sequence 9, Application US/10037243
; Publication No. US20030134352A1
; GENERAL INFORMATION:
; APPLICANT: Brookhaven Science Associates, LLC.
; APPLICANT: Prelimuth, Paul I
; APPLICANT: Zhang, Ylan-Biao
; APPLICANT: Howitt, Jason A
; TITLE OF INVENTION: Facilitating Protein Folding and Solubility by Use of Peptide Ext
; FILE REFERENCE: BSA 01-22
; CURRENT APPLICATION NUMBER: US/10/037,243
; CURRENT FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic T7B3 peptide
US-10-037-243-9
Query Match 100.0%; Score 27; DB 12; Length 44;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
DB 24 RTRGG 28
RESULT 4
US-09-897-898-12
; Sequence 12, Application US/09897898
; Patent No. US20020037303A1
; GENERAL INFORMATION:
; APPLICANT: DECKERS, HARM M.
; APPLICANT: VAN ROOIJEN, GIJS
; APPLICANT: BOOTHE, JOSEPH
; APPLICANT: COLL, JANIS
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
; FILE REFERENCE: 034547/0104
; CURRENT APPLICATION NUMBER: US/09/897,898
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/577,147
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/448,600
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/084,777
; PRIOR FILING DATE: 1998-05-27
; PRIOR APPLICATION NUMBER: 60/047,753
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: 60/047,779
; PRIOR FILING DATE: 1997-05-28
; PRIOR APPLICATION NUMBER: 60/075,863
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/075,864
; PRIOR FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Phascolin
; OTHER INFORMATION: promoter-trixh oleosin-phascolin terminator
US-09-897-898-12
Query Match 100.0%; Score 27; DB 9; Length 55;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RTRGG 5
DB 47 RTRGG 51
RESULT 5
US-09-897-898-20
; Sequence 20, Application US/09897898
; Patent No. US20020037303A1
; GENERAL INFORMATION:
; APPLICANT: DECKERS, HARM M.
; APPLICANT: VAN ROOIJEN, GIJS
; APPLICANT: BOOTHE, JOSEPH
; APPLICANT: COLL, JANIS
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
; FILE REFERENCE: 034547/0104
; CURRENT APPLICATION NUMBER: US/09/897,898
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/577,147

;; PRIOR FILING DATE: 2000-05-24
;; PRIOR APPLICATION NUMBER: 09/448,600
;; PRIOR FILING DATE: 1999-11-24
;; PRIOR APPLICATION NUMBER: 09/084,777
;; PRIOR FILING DATE: 1998-05-27
;; PRIOR APPLICATION NUMBER: 60/047,753
;; PRIOR FILING DATE: 1997-05-27
;; PRIOR APPLICATION NUMBER: 60/047,779
;; PRIOR FILING DATE: 1997-05-28
;; PRIOR APPLICATION NUMBER: 60/075,863
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/075,864
;; PRIOR FILING DATE: 1998-02-25
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 20
;; LENGTH: 55
;; TYPE: PRT
;; ORGANISM: Unknown Organism
;; FEATURE:
;; OTHER INFORMATION: Description of Unknown Organism: Phaseolin
;; OTHER INFORMATION: promoter-thioredoxin reductase oleosin-phaseolin
US-09-897-898-20

Query Match 100.0%; Score 27; DB 9; Length 55;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
|||||
DB 47 RTRGG 51

RESULT 6
US-09-893-525-3
;; Sequence 3, Application US/09893525
;; Publication No. US20030126631A1
;; GENERAL INFORMATION:
;; APPLICANT: Moloney, Maurice M.
;; APPLICANT: Van Rooijen, Gijb
;; TITLE OF INVENTION: Preparation of Heterologous Proteins on Oil Bodies
;; FILE REFERENCE: 9369-172
;; CURRENT APPLICATION NUMBER: US/09/893,525
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: US 09/210,843
;; PRIOR FILING DATE: 1998-12-15
;; PRIOR APPLICATION NUMBER: US 08/846,021
;; PRIOR FILING DATE: 1997-04-25
;; PRIOR APPLICATION NUMBER: US 08/366,783
;; PRIOR FILING DATE: 1994-12-30
;; PRIOR APPLICATION NUMBER: US 08/142,418
;; PRIOR FILING DATE: 1993-11-16
;; PRIOR APPLICATION NUMBER: US 07/659,835
;; PRIOR FILING DATE: 1991-02-22
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 3
;; LENGTH: 55
;; TYPE: PRT
;; ORGANISM: Arabidopsis thaliana
US-09-893-525-3

Query Match 100.0%; Score 27; DB 11; Length 55;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
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DB 47 RTRGG 51

RESULT 7

US-10-260-960-5
;; Sequence 5, Application US/10260960
;; Publication No. US20030059910A1
;; GENERAL INFORMATION:
;; APPLICANT: Moloney, Maurice
;; APPLICANT: Roelien, Joseph
;; TITLE OF INVENTION: Oil Bodies and Associated Proteins as Affinity Matrices
;; FILE REFERENCE: 9369-225
;; CURRENT APPLICATION NUMBER: US/10/260,960
;; CURRENT FILING DATE: 2002-10-01
;; PRIOR APPLICATION NUMBER: US 09/319,275
;; PRIOR FILING DATE: 1999-08-27
;; PRIOR APPLICATION NUMBER: US 08/767,026
;; PRIOR FILING DATE: 1997-12-16
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 5
;; LENGTH: 125
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Oleosin - Hirudin Fusion
US-10-260-960-5

Query Match 100.0%; Score 27; DB 15; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
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DB 47 RTRGG 51

RESULT 8
US-10-260-562-5
;; Sequence 5, Application US/10260562
;; Publication No. US20030096320A1
;; GENERAL INFORMATION:
;; APPLICANT: Moloney, Maurice
;; APPLICANT: Roelien, Gijb Van
;; TITLE OF INVENTION: Oil Bodies and Associated Proteins as Affinity Matrices
;; FILE REFERENCE: 9369-239
;; CURRENT APPLICATION NUMBER: US/10/260,562
;; CURRENT FILING DATE: 2002-10-01
;; PRIOR APPLICATION NUMBER: US 09/319,275
;; PRIOR FILING DATE: 1999-08-27
;; PRIOR APPLICATION NUMBER: US 08/767,026
;; PRIOR FILING DATE: 1997-12-16
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 5
;; LENGTH: 125
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Oleosin - Hirudin Fusion
US-10-260-562-5

Query Match 100.0%; Score 27; DB 15; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
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DB 47 RTRGG 51

RESULT 9
US-09-738-626-6573
;; Sequence 6573, Application US/09738626
;; Publication No. US20020197605A1

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: GENERAL INFORMATION:
: APPLICANT: NAKAGAWA, SATOSHI
: APPLICANT: MIZOGUCHI, HIROSHI
: APPLICANT: ANDO, SEIKO
: APPLICANT: HAYASHI, MIKIO
: APPLICANT: OCHIAI, KEIKO
: APPLICANT: YOKOI, HARUHIRO
: APPLICANT: TATEISHI, NAOKO
: APPLICANT: SENO, AKIHIRO
: APPLICANT: IKEDA, MASATO
: APPLICANT: OZAKI, AKIO
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
: FILE REFERENCE: 249-125
: CURRENT APPLICATION NUMBER: US/09/738,626
: CURRENT FILING DATE: 2000-12-18
: PRIOR APPLICATION NUMBER: JP 99/377484
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: JP 00/159162
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: JP 00/280988
: PRIOR FILING DATE: 2000-08-03
: NUMBER OF SEQ ID NOS: 7059
: SOFTWARE: PatentIn ver. 3.0
: SEQ ID NO 6573
: LENGTH: 146
: TYPE: PRT
: ORGANISM: Corynebacterium glutamicum
: US-09-738-626-6573

Query Match      100.0%; Score 27; DB 10; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTRGG 5
        |||||
DB      53 RTRGG 57

RESULT 10
US-09-747-155-173
: Sequence 173, Application US/09747155
: Patent No. US20020151692A1
: GENERAL INFORMATION:
: APPLICANT: Rouquier, Sylvie
: APPLICANT: Giorget, Dominique
: TITLE OF INVENTION: No. US20020151692A1 Polypeptides and Nucleic Acids Encoding Same
: FILE REFERENCE: 19904-008 (C009B883405)
: CURRENT APPLICATION NUMBER: US/09/747,155
: CURRENT FILING DATE: 2000-12-21
: PRIOR APPLICATION NUMBER: 60/171,746
: PRIOR FILING DATE: 1999-12-22
: NUMBER OF SEQ ID NOS: 431
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 173
: LENGTH: 162
: TYPE: PRT
: ORGANISM: Pan troglodytes
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (1)..(487)
: OTHER INFORMATION: Taxon = 9598; gene = PFR205; Accession DDBJ/EMBL/Genbank = AF1797
: US-09-747-155-173

Query Match      100.0%; Score 27; DB 10; Length 162;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTRGG 5
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DB      106 RTRGG 110

RESULT 11
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: US-09-897-898-9
: Sequence 9, Application US/09897898
: Patent No. US20020037303A1
: GENERAL INFORMATION:
: APPLICANT: DECKERS, HARM M.
: APPLICANT: VAN ROOIJEN, GIJS
: APPLICANT: BOOTHE, JOSEPH
: APPLICANT: GOL, JANIS
: APPLICANT: MOLONEY, MAURICE M.
: APPLICANT: DALMIA, BIPIN K.
: TITLE OF INVENTION: THIOREDUXIN AND THIOREDUXIN REDUCTASE CONTAINING OIL
: FILE REFERENCE: 034547/0104
: CURRENT APPLICATION NUMBER: US/09/897,898
: CURRENT FILING DATE: 2001-09-21
: PRIOR APPLICATION NUMBER: 09/577,147
: PRIOR FILING DATE: 2000-05-24
: PRIOR APPLICATION NUMBER: 09/448,600
: PRIOR FILING DATE: 1999-11-24
: PRIOR APPLICATION NUMBER: 09/084,777
: PRIOR FILING DATE: 1998-05-27
: PRIOR APPLICATION NUMBER: 60/047,753
: PRIOR FILING DATE: 1997-05-27
: PRIOR APPLICATION NUMBER: 60/047,779
: PRIOR FILING DATE: 1997-05-28
: PRIOR APPLICATION NUMBER: 60/075,863
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/075,864
: PRIOR FILING DATE: 1998-02-25
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 9
: LENGTH: 169
: TYPE: PRT
: ORGANISM: Unknown Organism
: FEATURE:
: OTHER INFORMATION: Description of Unknown Organism: Phasedlin
: OTHER INFORMATION: promoter-oleosin Trxh-phasedlin terminator
: US-09-897-898-9

Query Match      100.0%; Score 27; DB 9; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTRGG 5
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DB      47 RTRGG 51

RESULT 12
US-10-260-960-2
: Sequence 2, Application US/10260960
: Publication No. US20030059910A1
: GENERAL INFORMATION:
: APPLICANT: Moloney, Maurice
: APPLICANT: Boothe, Joseph
: APPLICANT: Rooijen, Gij's Van
: TITLE OF INVENTION: Oil Bodies and Associated Proteins as Affinity Matrices
: FILE REFERENCE: 9369-225
: CURRENT APPLICATION NUMBER: US/10/260,960
: CURRENT FILING DATE: 2002-10-01
: PRIOR APPLICATION NUMBER: US 09/319,275
: PRIOR FILING DATE: 1999-08-27
: PRIOR APPLICATION NUMBER: US 08/767,026
: PRIOR FILING DATE: 1997-12-16
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
: LENGTH: 173
: TYPE: PRT
: ORGANISM: Arabidopsis Thaliana
: US-10-260-960-2
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Query Match 100.0%; Score 27; DB 15; Length 173;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
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 DB 165 RTRGC 169

RESULT 13
 US-10-260-562-2
 : Sequence 2, Application US/10260562
 : Publication No. US20030096320A1
 : GENERAL INFORMATION:
 : APPLICANT: Moloney, Maurice
 : APPLICANT: Boonhe, Joseph
 : APPLICANT: Roeljen, Gijb Van
 : TITLE OF INVENTION: Oil Bodies and Associated Proteins as Affinity Matrices
 : FILE REFERENCE: 9369-239
 : CURRENT APPLICATION NUMBER: US/10/260,562
 : CURRENT FILING DATE: 2002-10-01
 : PRIOR APPLICATION NUMBER: US 09/319,275
 : PRIOR FILING DATE: 1998-08-27
 : PRIOR APPLICATION NUMBER: US 08/767,026
 : PRIOR FILING DATE: 1997-12-16
 : NUMBER OF SEQ ID NOS: 14
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 2
 : LENGTH: 173
 : TYPE: PRT
 : ORGANISM: Arabidopsis thaliana
 US-10-260-562-2

Query Match 100.0%; Score 27; DB 15; Length 173;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
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 DB 165 RTRGC 169

RESULT 14
 US-09-893-525-5
 : Sequence 5, Application US/09893525
 : Publication No. US20030126631A1
 : GENERAL INFORMATION:
 : APPLICANT: Moloney, Maurice M.
 : APPLICANT: Van Roeljen, Gijb
 : TITLE OF INVENTION: Preparation of Heterologous Proteins on Oil Bodies
 : FILE REFERENCE: 9369-172
 : CURRENT APPLICATION NUMBER: US/09/893,525
 : CURRENT FILING DATE: 2001-06-29
 : PRIOR APPLICATION NUMBER: US 09/210,843
 : PRIOR FILING DATE: 1998-12-15
 : PRIOR APPLICATION NUMBER: US 08/846,021
 : PRIOR FILING DATE: 1997-04-25
 : PRIOR APPLICATION NUMBER: US 08/366,783
 : PRIOR FILING DATE: 1994-12-30
 : PRIOR APPLICATION NUMBER: US 08/142,418
 : PRIOR FILING DATE: 1993-11-16
 : PRIOR APPLICATION NUMBER: US 07/659,835
 : PRIOR FILING DATE: 1991-02-22
 : NUMBER OF SEQ ID NOS: 42
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 5
 : LENGTH: 187
 : TYPE: PRT
 : ORGANISM: Brassica napus
 US-09-893-525-5

Query Match 100.0%; Score 27; DB 15; Length 187;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
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 DB 179 RTRGC 183

RESULT 15
 US-09-910-562-4
 : Sequence 4, Application US/09910562
 : Patent No. US20020098163A1
 : GENERAL INFORMATION:
 : APPLICANT: Zeng et al.
 : TITLE OF INVENTION: Human Tumor Necrosis Factor Receptors TR21 and TR22
 : FILE REFERENCE: PF530
 : CURRENT APPLICATION NUMBER: US/09/910,562
 : CURRENT FILING DATE: 2001-07-23
 : PRIOR APPLICATION NUMBER: 60/221,143
 : PRIOR FILING DATE: 2000-07-27
 : PRIOR APPLICATION NUMBER: 60/220,116
 : PRIOR FILING DATE: 2000-07-24
 : NUMBER OF SEQ ID NOS: 10
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 4
 : LENGTH: 194
 : TYPE: PRT
 : ORGANISM: homo sapiens
 US-09-910-562-4

Query Match 100.0%; Score 27; DB 9; Length 194;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
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 DB 1 RTRGC 5

Search completed: September 9, 2003, 23:47:28
 Job time : 47.875 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2003, 23:31:48 ; Search time 355 Seconds
(Without alignments)

12.816 Million cell updates/sec

Title: US-09-967-003-3

Perfect score: 1 RTKRG 5

Sequence: 2

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

Listing first 45 summaries

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32: /cgn2_6/ptodata1/paa/US106.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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2	27	100.0	5 25 US-09-967-003-3	Sequence 3, Appl1
3	27	100.0	10 28 US-10-287-043-2186	Sequence 2186, Ap
4	27	100.0	10 28 US-10-287-043-2188	Sequence 2188, Ap
5	27	100.0	19 6 US-08-222-626A-41	Sequence 41, Appl
6	27	100.0	19 14 US-09-009-843C-150	Sequence 150, App
7	27	100.0	19 14 US-09-009-843D-150	Sequence 150, App
8	27	100.0	32 1 PCT-US00-26524B-6856	Sequence 6856, Ap
9	27	100.0	32 27 US-10-106-698-6866	Sequence 6866, Ap
10	27	100.0	33 16 US-09-270-767-58721	Sequence 58721, A
11	27	100.0	33 16 US-09-270-849B-185516	Sequence 185516, A
12	27	100.0	34 20 US-09-617-682A-3655	Sequence 3655, Ap
13	27	100.0	36 13 US-08-948-538A-37	Sequence 37, Appl
14	27	100.0	37 1 PCT-US01-14827-12097	Sequence 12097, A
15	27	100.0	41 1 PCT-US01-01354-9822	Sequence 9822, Ap
16	27	100.0	41 22 US-09-764-905-9822	Sequence 9822, Ap
17	27	100.0	41 26 US-10-092-399-9822	Sequence 9822, Ap
18	27	100.0	43 20 US-09-617-682A-4434	Sequence 4434, Ap
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20	27	100.0	45 21 US-09-708-427-73722	Sequence 73722, A
21	27	100.0	47 30 US-10-437-963-179301	Sequence 179301, A
22	27	100.0	45 30 US-10-424-599-172648	Sequence 172648, A
23	27	100.0	50 1 PCT-US02-32727-20641	Sequence 20641, A
24	27	100.0	50 1 PCT-US02-32727-28946	Sequence 28946, A
25	27	100.0	50 20 US-09-617-682A-766	Sequence 766, App
26	27	100.0	50 25 US-09-978-825-20641	Sequence 20641, A
27	27	100.0	50 25 US-09-978-825-28946	Sequence 28946, A
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29	27	100.0	50 26 US-10-057-498-28946	Sequence 28946, A
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31	27	100.0	51 25 US-09-978-825-29223	Sequence 29223, A
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33	27	100.0	53 30 US-10-437-963-140895	Sequence 140895, A
34	27	100.0	54 20 US-09-688-052-3048	Sequence 3048, Ap
35	27	100.0	54 30 US-10-424-599-212139	Sequence 212139, A
36	27	100.0	55 12 US-08-846-021-3	Sequence 3, Appl1
37	27	100.0	55 23 US-09-893-525-3	Sequence 3, Appl1
38	27	100.0	55 23 US-09-897-425-3	Sequence 47, Appl1
39	27	100.0	55 23 US-09-897-425-47	Sequence 55, Appl1
40	27	100.0	55 23 US-09-897-425-55	Sequence 12, Appl1
41	27	100.0	55 23 US-09-897-898-12	Sequence 20, Appl1
42	27	100.0	55 23 US-09-897-898-12	Sequence 18, Appl1
43	27	100.0	55 26 US-10-006-038A-18	Sequence 26, Appl1
44	27	100.0	55 26 US-10-006-038A-26	Sequence 21, Appl1
45	27	100.0	55 26 US-10-032-201B-21	

ALIGNMENTS

RESULT 1

PCT-US00-06062-3

Sequence 3 Application PC/TUS0006062

GENERAL INFORMATION:

APPLICANT: Haddock, Jeffrey Lynn

APPLICANT: Blalock, James Edwin

APPLICANT: Pfister, Roswell Robert

APPLICANT: Villain, Matteo

TITLE OF INVENTION: Synthetic Complementary Peptides and

FILE REFERENCE: D6201PCT

CURRENT APPLICATION NUMBER: PCT/US00/06062

EARLIER FILING DATE: 2000-03-08

EARLIER APPLICATION NUMBER: US 60/123,409

EARLIER FILING DATE: 1999-03-09

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 3

LENGTH: 5

TYPE: PRT

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: amino acid sequence of complementary peptide

OTHER INFORMATION: inhibitor of neutrophils; used as monomer

PCT-US00-06062-3

Query Match 100.0%; Score 27; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTGG 5
DB 1 RTGG 5

RESULT 2
US-09-967-003-3
; Sequence 3, Application US/09967003
; GENERAL INFORMATION:
; APPLICANT: Haddox, Jeffrey
; APPLICANT: Pilster, Robert
; APPLICANT: Bialock, James
; APPLICANT: Matteo, Villain
; TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC
; FILE REFERENCE: 92750/57
; CURRENT APPLICATION NUMBER: US/09/967,003
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/521,365
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: US 60/123,409
; PRIOR FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: description of artificial sequence: amino-acid
; OTHER INFORMATION: sequence of complementary peptide inhibitor of
US-09-967-003-3

Query Match 100.0%; Score 27; DB 25; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTGG 5
DB 1 RTGG 5

RESULT 3
US-10-287-043-2186
; Sequence 2186, Application US/10287043
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from higher eukaryote genome sequen
; FILE REFERENCE: Higher eukaryote patent
; CURRENT APPLICATION NUMBER: US/10/287,043
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 3214
; SOFTWARE: Protpatent version 1.0
; SEQ ID NO 2186
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Saccharomyces Cerevisiae
; FEATURE:
; OTHER INFORMATION: Sequence located in YPL19C at 550-559 and may interact with Sequ
US-10-287-043-2186

Query Match 100.0%; Score 27; DB 28; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTGG 5

DB 4 RTGG 8

RESULT 4
US-10-287-043-2188
; Sequence 2188, Application US/10287043
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from higher eukaryote genome seq
; FILE REFERENCE: Higher eukaryote patent
; CURRENT APPLICATION NUMBER: US/10/287,043
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 3214
; SOFTWARE: Protpatent version 1.0
; SEQ ID NO 2188
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Saccharomyces Cerevisiae
; FEATURE:
; OTHER INFORMATION: Sequence located in YPL19C at 549-558 and may interact with 5
US-10-287-043-2188

Query Match 100.0%; Score 27; DB 28; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTGG 5
DB 5 RTGG 9

RESULT 5
US-08-222-626A-41
; Sequence 41, Application US/08222626A
; GENERAL INFORMATION:
; APPLICANT: Arai, Naoko
; APPLICANT: Masuda, Esteban S.
; APPLICANT: Tokumitsu, Hiroshi
; TITLE OF INVENTION: PURIFIED COMPONENTS OF MAMMALIAN
; TITLE OF INVENTION: TRANSCRIPTION REGULATION COMPLEXES, AND ANALOGS
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DMAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,626A
; FILING DATE: 04-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,061
; FILING DATE: 05-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/113,971
; FILING DATE: 30-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/088,998
; FILING DATE: 30-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/088,483
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0392K3
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-222-626A-41

Query Match 100.0%; Score 27; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
DB 2 RTRGG 6

RESULT 6
US-09-009-843C-150
Sequence 150, Application US/09009843C
GENERAL INFORMATION:
APPLICANT: Arai, Naoko
APPLICANT: Masuda, Esteban S.
APPLICANT: Tokumitsu, Hiroshi
TITLE OF INVENTION: PURIFIED COMPONENTS OF MAMMALIAN
TRANSCRIPTION REGULATION COMPLEXES, AND ANALOGS
NUMBER OF SEQUENCES: 266
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30; #2.0; and
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,843C
FILING DATE: 20-JAN-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/222,626
FILING DATE: 04-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,061
FILING DATE: 05-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/113,971
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,998
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,483
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0392K3B
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 150:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-009-843C-150

Query Match 100.0%; Score 27; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
DB 2 RTRGG 6

RESULT 7
US-09-009-843D-150
Sequence 150, Application US/09009843D
GENERAL INFORMATION:
APPLICANT: Arai, Naoko
APPLICANT: Masuda, Esteban S.
APPLICANT: Tokumitsu, Hiroshi
TITLE OF INVENTION: PURIFIED COMPONENTS OF MAMMALIAN
TRANSCRIPTION REGULATION COMPLEXES, AND ANALOGS
NUMBER OF SEQUENCES: 266
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30; #2.0; and
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,843D
FILING DATE: 20-JAN-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/222,626
FILING DATE: 04-APR-1994
APPLICATION NUMBER: US 08/148,061
FILING DATE: 05-NOV-1993
APPLICATION NUMBER: US 08/113,971
FILING DATE: 30-AUG-1993
APPLICATION NUMBER: US 08/099,998
FILING DATE: 30-JUL-1993
APPLICATION NUMBER: US 08/088,483
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0392K3B
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 150:
US-09-009-843D-150
Query Match 100.0%; Score 27; DB 14; Length 19;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
Db 2 RTRGG 6

RESULT 8
PCT-US00-26524B-6856
Sequence 6856, Application PC/7US0026524B
GENERAL INFORMATION:
APPLICANT: Birse et. al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005PCT
CURRENT APPLICATION NUMBER: PCT/US00/26524B
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6856
LENGTH: 32
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (117)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (22)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (23)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (25)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US00-26524B-6856

Query Match 100.0%; Score 27; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
Db 26 RTRGG 30

RESULT 9
US-10-106-698-6866
Sequence 6866, Application US/10106698
GENERAL INFORMATION:
APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 6866
LENGTH: 32
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: MISC_FEATURE
LOCATION: (117)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (22)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (23)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (25)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6866

Query Match 100.0%; Score 27; DB 27; Length 32;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
Db 26 RTRGG 30

RESULT 10
US-09-270-767-58721
Sequence 58721, Application US/09270767
GENERAL INFORMATION:
APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58721
LENGTH: 33
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-58721

Query Match 100.0%; Score 27; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
Db 9 RTRGG 13

RESULT 11
US-09-270-849B-185516
Sequence 185516, Application US/09270849B
GENERAL INFORMATION:
APPLICANT: Swimmer et al.

TITLE OF INVENTION: Insect genome survey devices
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 185516
LENGTH: 33
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-185516

Query Match 100.0%; Score 27; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5

Db 9 RTRGG 13

RESULT 12
US-09-617-682A-3655

Sequence 3655, Application US/09617682A
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVNER, Vyacheslav
TITLE OF INVENTION: Sequence-determined DNA fragments and corresponding polypeptides
TITLE OF INVENTION: thereby
FILE REFERENCE: 2750-1063P
CURRENT APPLICATION NUMBER: US/09/617,682A
CURRENT FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 16871
SEQ ID NO 3655
LENGTH: 34
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..34
OTHER INFORMATION: xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..34
OTHER INFORMATION: Ceres Seq. ID 1351169
US-09-617-682A-3655

Query Match 100.0%; Score 27; DB 20; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
Db 7 RTRGG 11

RESULT 13
US-08-948-538A-37

Sequence 37, Application US/08948538A
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANDOS, EDWARD N.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROPE, STEVEN D.
TITLE OF INVENTION: NOVEL ASPARTYL PROTEASE
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING AND
TITLE OF INVENTION: TREATING DISEASES OF THE LUNG
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,538A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6184.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
US-08-948-538A-37

Query Match 100.0%; Score 27; DB 13; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
Db 18 RTRGG 22

RESULT 14
PCT-US01-14827-12097

Sequence 12097, Application PC/TUS0114827
GENERAL INFORMATION:
APPLICANT: HySeq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-104
CURRENT APPLICATION NUMBER: PCT/US01/14827
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 16102
SOFTWARE: Custom
SEQ ID NO 12097
LENGTH: 37
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-14827-12097

Query Match 100.0%; Score 27; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
Db 3 RTRGG 7

RESULT 15
PCT-US01-01354-9822

Sequence 9822, Application PC/TUS0101354
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC004PCT
CURRENT APPLICATION NUMBER: PCT/US01/01354
CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 42506
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9822
LENGTH: 41
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-01354-9822

Query Match 100.0%; Score 27; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	RTRCG	5						
Db	19	RTRCG	23						

Search completed: September 9, 2003, 23:45:44
Job time : 356 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2003, 23:32:23 ; Search time 10.625 Seconds
(without alignments)
4.496 Million cell updates/sec

Title: US-09-967-003-3

Perfect score: 27

Sequence: 1 RTRGC 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 47124 seqs, 9554045 residues

Total number of hits satisfying chosen parameters: 47124

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database: Pending Patents_AA_New.*

1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	277	5	US-09-674-546A-1227
2	27	100.0	537	1	PCT-US03-24505-26
3	27	100.0	537	7	US-60-485-450-1577
4	24	88.9	149	7	US-60-495-114-1690
5	24	88.9	530	5	US-09-581-286A-499
6	24	88.9	599	5	US-09-581-286A-498
7	24	88.9	614	5	US-09-581-286A-364
8	24	88.9	835	7	US-60-490-890-896
9	24	88.9	2705	1	PCT-US03-21510-97
10	23	85.2	26	5	US-09-592-617C-4
11	23	85.2	27	5	US-09-592-617C-38
12	23	85.2	193	7	US-60-490-890-1518
13	23	85.2	194	7	US-60-487-610-1656
14	23	85.2	235	1	PCT-US02-29560A-337
15	23	85.2	311	1	PCT-US02-29560A-338
16	23	85.2	321	5	US-09-897-516A-6988
17	23	85.2	402	5	US-09-721-870-46
18	23	85.2	402	6	US-10-650-467-46
19	23	85.2	420	7	US-60-478-777-12
20	23	85.2	443	7	US-60-478-777-10
21	23	85.2	471	5	US-09-897-516A-7981
22	23	85.2	495	5	US-09-976-838-117
23	23	85.2	669	7	US-60-485-450-1584
24	23	85.2	707	7	US-60-485-450-1585
25	23	85.2	748	7	US-60-487-610-2629
26	23	85.2	748	7	US-60-495-114-2124

27	23	85.2	748	7	US-60-495-114-2125	Sequence 2125, Ap
28	23	85.2	926	5	US-09-897-516A-6173	Sequence 6173, Ap
29	23	85.2	997	7	US-60-487-610-2367	Sequence 2367, Ap
30	23	85.2	1007	7	US-60-485-450-1484	Sequence 1484, Ap
31	23	85.2	1047	7	US-60-490-890-2725	Sequence 2725, Ap
32	23	85.2	1047	7	US-60-483-917-2	Sequence 2, Appl
33	23	85.2	1047	7	US-60-487-610-1574	Sequence 1574, Ap
34	23	85.2	1152	5	US-09-592-617C-43	Sequence 43, Appl
35	23	85.2	1174	7	US-60-483-917-4	Sequence 4, Appl
36	23	85.2	2296	7	US-60-487-610-1850	Sequence 1850, Ap
37	23	85.2	2355	7	US-60-487-610-1848	Sequence 1848, Ap
38	23	85.2	2386	7	US-60-487-610-1851	Sequence 1851, Ap
39	23	85.2	2427	7	US-60-487-610-1852	Sequence 1852, Ap
40	23	85.2	2477	7	US-60-487-610-1849	Sequence 1849, Ap
41	22	81.5	129	5	US-09-805-290A-18	Sequence 18, Appl
42	22	81.5	144	5	US-09-897-516A-6833	Sequence 6833, Ap
43	22	81.5	158	7	US-60-490-890-958	Sequence 958, Ap
44	22	81.5	167	6	US-10-375-932-117	Sequence 117, Ap
45	22	81.5	167	6	US-10-375-932-122	Sequence 122, Ap

ALIGNMENTS

RESULT 1
US-09-674-546A-1227
Sequence 1227, Application US/09674546A
GENERAL INFORMATION:
APPLICANT: Institute for Genomic Research
TITLE OF INVENTION: Neisseria Meningitidis Antigens and Compositions
FILE REFERENCE: CHR-0334
CURRENT APPLICATION NUMBER: US/09/674,546A
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 3264
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1227
LENGTH: 277
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-674-546A-1227

Query Match 100.0% Score 27; DB 5; Length 277;
Best Local Similarity 100.0% Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 62 RTRGC 66
OY 1 RTRGC 5
PCT-US03-24505-26
Sequence 26, Application PC/TUS0324505
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: ME2153S AS MODIFIERS OF THE p21 OR p53 PATHWAY AND METHODS OF
FILE REFERENCE: EX03-053C-PC
CURRENT APPLICATION NUMBER: PCT/US03/24505
CURRENT FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: US 60/401,701
PRIOR FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 60/411,017
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/437,107
PRIOR FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26
LENGTH: 537
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-24505-26

Query Match 100.0%; Score 27; DB 1; Length 537;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTGCG 5
 |||||
 DB 77 RTGCG 81

RESULT 3

US-60-485-450-1577
 : Sequence 1577, Application US/60485450
 : GENERAL INFORMATION:

APPLICANT: CARGILL, Michele
 : APPLICANT: CHANG, Sheng-Yung
 : TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 : TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
 : TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
 : FILE REFERENCE: CL001470
 : CURRENT APPLICATION NUMBER: US/60/485,450
 : CURRENT FILING DATE: 2003-07-09
 : NUMBER OF SEQ ID NOS: 47859
 : SOFTWARE: FASTSEQ for Windows Version 4.0
 : SEQ ID NO 1577
 : LENGTH: 537
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-60-485-450-1577

Query Match 100.0%; Score 27; DB 7; Length 537;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTGCG 5
 |||||
 DB 77 RTGCG 81

RESULT 4

US-60-495-114-1690
 : Sequence 1690, Application US/60495114
 : GENERAL INFORMATION:

APPLICANT: CARGILL, Michele
 : TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
 : TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
 : FILE REFERENCE: CL001480
 : CURRENT APPLICATION NUMBER: US/60/495,114
 : CURRENT FILING DATE: 2003-08-15
 : NUMBER OF SEQ ID NOS: 91238
 : SOFTWARE: FASTSEQ for Windows Version 4.0
 : SEQ ID NO 1690
 : LENGTH: 149
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-60-495-114-1690

Query Match 88.9%; Score 24; DB 7; Length 149;
 Best Local Similarity 80.0%; Pred. No. 68;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTGCG 5
 |||||
 DB 126 KTRGG 130

RESULT 5

US-09-581-286A-499
 : Sequence 499, Application US/09581286A
 : GENERAL INFORMATION:
 : APPLICANT: ROSS, BRUCE C.

APPLICANT: BARR, IAN G.
 : APPLICANT: PATTERSON, MICHELLE A.
 : APPLICANT: AGIUS, CATHERINE T.
 : APPLICANT: ROTHEL, LINDA J.
 : APPLICANT: MARGETTS, MAL B.
 : APPLICANT: HOCKING, DIANNA M.
 : APPLICANT: WEBB, ELIZABETH A.
 : TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
 : FILE REFERENCE: 4137-3
 : CURRENT APPLICATION NUMBER: US/09/581,286A

CURRENT FILING DATE: 2000-06-28
 : PRIOR APPLICATION NUMBER: PCT/AU98/01023
 : PRIOR FILING DATE: 1998-12-10
 : PRIOR APPLICATION NUMBER: AU PP 0839
 : PRIOR FILING DATE: 1997-12-10
 : PRIOR APPLICATION NUMBER: AU PP 1182
 : PRIOR FILING DATE: 1997-12-31
 : PRIOR APPLICATION NUMBER: AU PP 1846
 : PRIOR FILING DATE: 1998-01-30
 : PRIOR APPLICATION NUMBER: AU PP 2264
 : PRIOR FILING DATE: 1998-03-10
 : PRIOR APPLICATION NUMBER: AU PP 2911
 : PRIOR FILING DATE: 1998-04-09
 : PRIOR APPLICATION NUMBER: AU PP 3128
 : PRIOR FILING DATE: 1998-04-23
 : PRIOR APPLICATION NUMBER: AU PP 3338
 : PRIOR FILING DATE: 1998-05-05
 : PRIOR APPLICATION NUMBER: AU PP 3654
 : PRIOR FILING DATE: 1998-05-22
 : PRIOR APPLICATION NUMBER: AU PP 4917
 : PRIOR FILING DATE: 1998-07-29
 : Remaining prior Application data removed - See file Wrapper or PALM.
 : NUMBER OF SEQ ID NOS: 721
 : SOFTWARE: PatentIn version 3.2
 : SEQ ID NO 499
 : LENGTH: 550
 : TYPE: PRT
 : ORGANISM: Porphyromonas gingivalis
 : US-09-581-286A-499

Query Match 88.9%; Score 24; DB 5; Length 550;
 Best Local Similarity 80.0%; Pred. No. 2,6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTGCG 5
 |||||
 DB 88 RTGCG 92

RESULT 6

US-09-581-286A-498
 : Sequence 498, Application US/09581286A
 : GENERAL INFORMATION:

APPLICANT: ROSS, BRUCE C.
 : APPLICANT: BARR, IAN G.
 : APPLICANT: PATTERSON, MICHELLE A.
 : APPLICANT: AGIUS, CATHERINE T.
 : APPLICANT: ROTHEL, LINDA J.
 : APPLICANT: MARGETTS, MAL B.
 : APPLICANT: HOCKING, DIANNA M.
 : APPLICANT: WEBB, ELIZABETH A.
 : TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
 : FILE REFERENCE: 4137-3
 : CURRENT APPLICATION NUMBER: US/09/581,286A
 : CURRENT FILING DATE: 2000-06-28
 : PRIOR APPLICATION NUMBER: PCT/AU98/01023
 : PRIOR FILING DATE: 1998-12-10
 : PRIOR APPLICATION NUMBER: AU PP 0839
 : PRIOR FILING DATE: 1997-12-10
 : PRIOR APPLICATION NUMBER: AU PP 1182
 : PRIOR FILING DATE: 1997-12-31
 : PRIOR APPLICATION NUMBER: AU PP 1846
 : PRIOR FILING DATE: 1998-01-30

PRIOR APPLICATION NUMBER: AU PP 2264
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: AU PP 2911
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: AU PP 3128
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: AU PP 3338
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: AU PP 3654
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: AU PP 4917
PRIOR FILING DATE: 1998-07-29
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 721
SOFTWARE: PatentIn version 3.2
SEQ ID NO 498
LENGTH: 599
TYPE: PRT
ORGANISM: Porphyromonas gingivalis
US-09-581-286A-498

Query Match 88.9%; Score 24; DB 5; Length 599;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTRGC 5
DB 137 RTRGC 141

RESULT 7
US-09-581-286A-364
Sequence 364, Application US/09581286A
GENERAL INFORMATION:
APPLICANT: ROSS, BRUCE C.
APPLICANT: BARR, IAN G.
APPLICANT: PATTERSON, MICHELLE A.
APPLICANT: AGIUS, CATHERINE T.
APPLICANT: ROTHEL, LINDA J.
APPLICANT: MARGETTS, MAL B.
APPLICANT: HOCKING, DIANNA M.
APPLICANT: WEBB, ELIZABETH A.
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
FILE REFERENCE: 4137-3
CURRENT APPLICATION NUMBER: US/09/581,286A
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: PCT/AU98/01023
PRIOR FILING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: AU PP 0839
PRIOR FILING DATE: 1997-12-10
PRIOR APPLICATION NUMBER: AU PP 1182
PRIOR FILING DATE: 1997-12-31
PRIOR APPLICATION NUMBER: AU PP 1846
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: AU PP 2264
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: AU PP 2911
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: AU PP 3128
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: AU PP 3338
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: AU PP 3654
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: AU PP 4917
PRIOR FILING DATE: 1998-07-29
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 721
SOFTWARE: PatentIn version 3.2
SEQ ID NO 364
LENGTH: 614
TYPE: PRT
ORGANISM: Porphyromonas gingivalis

US-09-581-286A-364

Query Match 88.9%; Score 24; DB 5; Length 614;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGC 5
DB 152 RTRGC 156

RESULT 8
US-60-490-890-896
Sequence 896, Application US/60490890
GENERAL INFORMATION:
APPLICANT: LI, Martha
APPLICANT: Rupnow, Brent A.
APPLICANT: Webster, Kevin R.
APPLICANT: Jackson, Donald
APPLICANT: Wong, Tai W.
TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
FILE REFERENCE: D0310 PSP
CURRENT APPLICATION NUMBER: US/60/490,890
PRIOR FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 2779
SOFTWARE: PatentIn version 3.2
SEQ ID NO 896
LENGTH: 835
TYPE: PRT
ORGANISM: Homo sapiens
US-60-490-890-896

Query Match 88.9%; Score 24; DB 7; Length 835;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGC 5
DB 825 RTRGC 829

RESULT 9
PCT-US03-21510-97
Sequence 97, Application PC/TUS0321510
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: AP215 AS MODIFIERS OF THE p21 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX03-046C-PC
CURRENT APPLICATION NUMBER: PCT/US03/21510
PRIOR FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US 60/394,795
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/401,739
PRIOR FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 60/411,010
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/437,158
PRIOR FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.2
SEQ ID NO 97
LENGTH: 2705
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-21510-97

Query Match 88.9%; Score 24; DB 1; Length 2705;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGC 5
DB 2175 RTRGC 2179

```
RESULT 10
US-09-592-617C-4
; Sequence 4, Application US/09592617C
; GENERAL INFORMATION:
; APPLICANT: Arnsout, M. Armin
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS
; FILE REFERENCE: 00786-267002
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 08/280,167
; PRIOR FILING DATE: 1999-01-30
; PRIOR APPLICATION NUMBER: US 08/216,081
; PRIOR FILING DATE: 1994-03-21
; PRIOR APPLICATION NUMBER: US 07/637,830
; PRIOR FILING DATE: 1991-01-04
; PRIOR APPLICATION NUMBER: US 07/539,842
; PRIOR FILING DATE: 1990-06-18
; PRIOR APPLICATION NUMBER: US 07/212,573
; PRIOR FILING DATE: 1988-06-28
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-592-617C-4

Query Match      85.2%; Score 23; DB 5; Length 26;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
    :||||
Db 3 QTRGG 7

RESULT 11
US-09-592-617C-38
; Sequence 38, Application US/09592617C
; GENERAL INFORMATION:
; APPLICANT: Arnsout, M. Armin
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS
; FILE REFERENCE: 00786-267002
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 08/280,167
; PRIOR FILING DATE: 1999-01-30
; PRIOR APPLICATION NUMBER: US 08/216,081
; PRIOR FILING DATE: 1994-03-21
; PRIOR APPLICATION NUMBER: US 07/637,830
; PRIOR FILING DATE: 1991-01-04
; PRIOR APPLICATION NUMBER: US 07/539,842
; PRIOR FILING DATE: 1990-06-18
; PRIOR APPLICATION NUMBER: US 07/212,573
; PRIOR FILING DATE: 1988-06-28
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-592-617C-38

Query Match      85.2%; Score 23; DB 5; Length 27;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
    :||||
Db 4 QTRGG 8

RESULT 12
US-60-490-890-1518
; Sequence 1518, Application US/60490890
; GENERAL INFORMATION:
; APPLICANT: Li, Martha
; APPLICANT: Rupnow, Brent A.
; APPLICANT: Webster, Kevin R.
; APPLICANT: Jackson, Donald
; APPLICANT: Wong, Tai W.
; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
; FILE REFERENCE: D0310 PSP
; CURRENT APPLICATION NUMBER: US/60/490,890
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 2779
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1518
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-490-890-1518

Query Match      85.2%; Score 23; DB 7; Length 193;
Best Local Similarity 80.0%; Pred. No. 1,4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
    :||||
Db 4 RSRGG 8

RESULT 13
US-60-487-610-1656
; Sequence 1656, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: C1001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1656
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1656

Query Match      85.2%; Score 23; DB 7; Length 194;
Best Local Similarity 80.0%; Pred. No. 1,4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
    :||||
Db 131 QTRGG 135

RESULT 14
PCT-US02-29560A-337
; Sequence 337, Application PC/TUS0229560A
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
```

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; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560A
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 337
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29560A-337

```

Query Match

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Best Local Similarity 85.2%; Score 23; DB 1; Length 235;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 RTRGG 5
   :||||

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```

Db 162 QTRGG 166

```

RESULT 15

```

PCT-US02-29560A-338
; Sequence 338, Application PC/TUS0229560A
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezl, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560A
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29560A-338

```

Query Match

```

Best Local Similarity 85.2%; Score 23; DB 1; Length 311;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RTRGG 5
   :||||

```

```

Db 238 QTRGG 242

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Search completed: September 9, 2003, 23:46:06
 Job time : 11.625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2003, 23:28:28 : Search time 31.25 Seconds
(without alignments)
15.387 Million cell updates/sec

Title: US-09-967-003-3

Perfect score: 27

Sequence: 1 RTRG 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR_76:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	64	2	SI4856
2	27	100.0	113	2	SI56448
3	27	100.0	113	2	H91278
4	27	100.0	113	2	H86119
5	27	100.0	114	2	AF1055
6	27	100.0	127	2	D69125
7	27	100.0	129	2	A64384
8	27	100.0	145	2	E81222
9	27	100.0	145	2	A81992
10	27	100.0	173	1	S22538
11	27	100.0	199	1	VCV083
12	27	100.0	199	2	SI0986
13	27	100.0	200	2	S45591
14	27	100.0	202	2	T49800
15	27	100.0	208	2	T16343
16	27	100.0	240	2	SI0406
17	27	100.0	245	2	A97073
18	27	100.0	245	2	G84886
19	27	100.0	256	2	AD1480
20	27	100.0	256	2	A11119
21	27	100.0	258	2	C69632
22	27	100.0	259	2	G83755
23	27	100.0	262	2	AD2819
24	27	100.0	294	2	T29212
25	27	100.0	295	2	E97597
26	27	100.0	310	2	C60245
27	27	100.0	313	2	D58866
28	27	100.0	320	2	E71095
29	27	100.0	353	1	JQ1946

30	27	100.0	360	2	G86435	protein F17F8.7 (1
31	27	100.0	379	2	S55900	DNA-like protein
32	27	100.0	379	2	T41633	psi protein - flss
33	27	100.0	384	2	H87019	probable glycosyl
34	27	100.0	422	2	T06388	alpha-galactosidas
35	27	100.0	444	2	B75348	glucose-1-phosphat
36	27	100.0	486	2	T48119	hypothetical prote
37	27	100.0	487	2	T45982	hypothetical prote
38	27	100.0	492	2	T36429	probable iron-sulf
39	27	100.0	510	2	T49308	hypothetical prote
40	27	100.0	527	2	D70595	probable ATP-depen
41	27	100.0	534	1	A44991	protein-tyrosine k
42	27	100.0	534	1	S33568	protein-tyrosine k
43	27	100.0	534	2	E87278	sensor histidine k
44	27	100.0	537	1	A43806	protein-tyrosine k
45	27	100.0	537	1	TVHUSY	protein-tyrosine k

ALIGNMENTS

RESULT 1
SI4856
hypothetical protein 3 - yeast (*Pichia angusta*)
C:Species: *Pichia angusta*
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Apr-2000
C:Accession: SI4856
R:Krutlina, A.I., Seragina, S.A., Tikhomirova, L.P., Kryukov, V.M.
submitted to the EMBL Data Library, April 1991
A:Description: Nucleotide sequence of *Hansenula polymorpha* DNA region complementing 1
A:Reference number: SI4854
A:Accession: SI4856
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-64 <RND>
A:Cross-references: EMBL:X58862; NID:92762; PIDD:CAA1667.1; PTD:92765

Query Match 100.0%; Score 27; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 12 RTRG 16
OY 1 RTRG 5
DB 12 RTRG 16
RESULT 2
S56448
hypothetical 12.9K protein (msra-chpbl intergenic region) - *Escherichia coli* (strain
N:Alternate names: hypothetical protein o113
C:Species: *Escherichia coli*
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 01-Mar-2002
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
C:Accession: S56448; A65234
A:Reference number: S56448; MUID:9534362; PMID:7610040
A:Title: Analysis of the *Escherichia coli* genome VI: DNA sequence of the region from
A:Reference number: S56314; MUID:9534362; PMID:7610040
A:Accession: S56448
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-113 <SNUR>
A:Cross-references: EMBL:U14003; NID:91263172; PIDD:AAA97119.1; PTD:9537064
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A:Rose, D.J.; Mau, B.; Sho, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A65234
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-113 <BIAT>
A:Cross-references: GB:AE000493; GB:U00096; NID:92367360; PIDD:AACT7179.1; PTD:q17906

A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: ytfP

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 113;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
DB 70 RTRGG 74

RESULT 3

hypothetical protein ECs5200 [imported] - Escherichia coli (strain O157:H7, substrain R)

C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C:Accession: H91278
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gatawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: H91278
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-113 <NAV>
A:Cross-references: GB:BA000007; PIDN:BA938623.1; PID:g13364677; GSPDB:GNO0154

A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs5200

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 113;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
DB 70 RTRGG 74

RESULT 4

hypothetical protein ytfP [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: H86119
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Miller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimantanta, E.; Potlamosis, K.; Apodaca, Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: H86119
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-113 <STO>
A:Cross-references: GB:AE005174; NID:912519221; PIDN:AA659420.1; GSPDB:GNO0145; UWGP:258

A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ytfP

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 113;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
DB 70 RTRGG 74

RESULT 5

AF1055

conserved hypothetical protein ytfP [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typh
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AF1055
R:Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Church th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Parr , S.; Moutle, S.; O'Garra, P. Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AF1055
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-114 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD06891.1; PID:g16505539; GSPDB:GNO0176

C:Genetics:
A:Gene: ytfP

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 114;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
DB 70 RTRGG 74

RESULT 6

ribosomal protein S8 - Methanobacterium thermoautotrophicum (strain Delta H)

C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 13-Aug-1999

C:Accession: D69125
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: D69125
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-127 <MTH>
A:Cross-references: GB:AE000807; GB:AE000666; NID:92621239; PIDN:AA84713.1; PID:9262

A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH207
C:Superfamily: rat ribosomal protein S8

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 127;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
DB 46 RTRGG 50

RESULT 7

ribosomal protein S8 er - Methanococcus jannaschii

C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: A64384
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak , Reich, C.I.; Overbeek, R.; Kirsch, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: A64384
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-129 <BUL>
 A:Cross-references: GB:U67514; GB:L77117; NID:92826304; PIDN:AAB98667.1; PID:91591387; P:91591387
 C:Genetics:
 A:Map position: FORS99257-599646
 C:Superfamily: rat ribosomal protein S8
 C:Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 27; DB 2; Length 129;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RTRGG 5
 Db 48 RTRGG 52

RESULT 8
 E81222
 hypothetical protein NMB0247 [imported] - Neisseria meningitidis (strain MC58 serogroup C)
 C:Species: Neisseria meningitidis
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C:Accession: E81222
 R:Retelien, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, R.E.; Eisen, J.A.; Hickey, E.R.; Halt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Venter, A.; Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755; PMID:10710307
 A:Accession: E81222
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-145 <REV>
 A:Cross-references: GB:AE002381; GB:AE002098; NID:97225455; PIDN:AAAF40701.1; PID:9722546
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB0247
 C:Superfamily: Neisseria meningitidis hypothetical protein NMB0247

Query Match 100.0%; Score 27; DB 2; Length 145;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RTRGG 5
 Db 91 RTRGG 95

RESULT 9
 A81992
 hypothetical protein NMA0013 [imported] - *Neisseria meningitidis* (strain Z2491 serogroup C)
 C:Species: *Neisseria meningitidis*
 C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: A81992
 R:Parikh, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jagals, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, A.; Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A:Reference number: A81775; MUID:20222356; PMID:10761919
 A:Accession: A81992
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-145 <PAR>
 A:Cross-references: GB:AL162752; GB:AL157959; NID:97378778; PIDN:CA83333.1; PID:9737878
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: NMA0013
 C:Superfamily: *Neisseria meningitidis* hypothetical protein NMB0247

Query Match 100.0%; Score 27; DB 2; Length 145;

Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RTRGG 5
 Db 91 RTRGG 95

RESULT 10
 S22538
 oleosin, 18.5K - *Arabidopsis thaliana*
 N:Alternate names: protein F13M23.280
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S22538; T05535; S22143
 R:van Rooijen, G.J.H.; Terling, L.I.; Moloney, M.M. Plant Mol. Biol. 18, 1177-1179, 1992
 A:Title: Nucleotide sequence of an *Arabidopsis thaliana* oleosin gene.
 A:Reference number: S22538; MUID:92288310; PMID:1600152
 A:Accession: S22538
 A:Molecule type: DNA
 A:Residues: 1-173 <ROO>
 A:Cross-references: EMBL:X62353; NID:916404; PIDN:CAAA44225.1; PID:916405
 A:Experimental source: cv. Columbia
 R:Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hohnsels, J.; Mewes, H.W.; Mayer, A.; Reference number: Z15419
 A:Accession: T05535
 A:Molecule type: DNA
 A:Residues: 1-173 <BEV>
 A:Cross-references: EMBL:AL035523
 A:Experimental source: cultivar Columbia; BAC clone F13M23
 C:Genetics:
 A:Map position: 4
 A:Introns: 118/2
 A:Note: F13M23.280
 C:Superfamily: oleosin
 C:Keywords: seed

Query Match 100.0%; Score 27; DB 1; Length 173;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RTRGG 5
 Db 165 RTRGG 169

RESULT 11
 VCVOB3
 coat protein - barley yellow dwarf virus (strain MAV-PS1)
 C:Species: barley yellow dwarf virus, BYDV
 C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jun-2000
 C:Accession: J01411
 R:Remy, P.P.; Vincent, J.R.; Kawata, E.E.; Lei, C.H.; Lister, R.M.; Larkins, B.A. J. Gen. Virol. 73, 487-492, 1992
 A:Title: Nucleotide sequence analysis of the genomes of the MAV-PS1 and P-PAV isolat
 A:Reference number: J01409; MUID:92166764; PMID:1538199
 A:Accession: J01411
 A:Molecule type: genomic RNA
 A:Residues: 1-199 <UNB>
 A:Cross-references: GB:D11028; DDBJ:D01213; NID:9221084; PIDN:BA01781.1; PID:922108
 C:Superfamily: potato leaf roll virus coat protein; potato leaf roll virus coat prot
 C:Keywords: coat protein
 F:1-199/Domain: potato leaf roll virus coat protein homology <COP>

Query Match 100.0%; Score 27; DB 1; Length 199;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RTRGG 5
 Db 44 RTRGG 48

RESULT 12

S10986

coat protein - barley yellow dwarf virus (isolate MAV)

N:Alternate names: capsid protein

C:Species: barley yellow dwarf virus, BYDV

C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 20-Sep-1999

C:Accession: S10986

R:Rizzo, T.M.; Gray, S.M.

Nucleic Acids Res. 18, 4625, 1990

A:Title: Cloning and sequence analysis of a cDNA encoding the capsid protein of the MAV

A:Reference number: S10986; PMID:90356431; PMID:2388853

A:Accession: S10986

A:Molecule type: genomic RNA

A:Residues: 1-199 <RT2>

A:Cross-references: EMBL:X53174; NID:g60519; PIDN:CAA3735.1; PID:g60520

C:Superfamily: potato leaf roll virus coat protein; potato leaf roll virus coat protein

C:Keywords: coat protein

F:1-199/Domain: potato leaf roll virus coat protein homology <COP>

Query Match

100.0%; Score 27; DB 2; Length 199;

Best Local Similarity 100.0%; Pred. No. 82;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTGG 5

DB 44 RTGG 48

RESULT 13

S45591

ribosomal protein S8.e, cytosolic - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YBL06.05; protein YBL0613; protein YBL072c; protein YER102w;

C:Species: Saccharomyces cerevisiae

C>Date: 19-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 23-Mar-2001

C:Accession: S45591; S45808; S50605; S11250; A36590; S38421

R:Logghe, M.; Molemans, F.; Piers, W.; Contreras, R.

Yeast 10, 1093-1100, 1994

A:Title: The two genes encoding yeast ribosomal protein S8 reside on different chromosomes

A:Reference number: S45588; PMID:95084636; PMID:7992509

A:Accession: S45591

A:Molecule type: DNA

A:Residues: 1-200 <LOG>

A:Cross-references: EMBL:Z26879; NID:g407519; PIDN:CAA81525.1; PID:g407523

R:Contreras, R.; Piers, W.; Logghe, M.; Molemans, F.

submitted to the Protein Sequence Database, August 1994

A:Reference number: S45802

A:Accession: S45808

A:Molecule type: DNA

A:Residues: 1-200 <CON>

A:Cross-references: EMBL:Z35833; GSPDB:GN00002; MIPS:YBL072c; NID:g536114; PIDN:CAA84893

A:Genetics: CH2

R:Dietrich, F.S.

submitted to the EMBL Data Library, December 1994

A:Description: The sequence of S. cerevisiae cosmid 9747, 8198, 9781, and lambda clones

A:Reference number: S50436

A:Accession: S50605

A:Molecule type: DNA

A:Residues: 1-200 <DIE>

A:Cross-references: EMBL:U18839; NID:g603113; PIDN:AA64657.1; PID:g603340; GSPDB:GN0000

A:Genetics: CH5

R:Okada, E.; Higo, K.I.; Itoh, T.

Mol. Gen. Genet. 195, 544-546, 1984

A:Title: Yeast ribosomal proteins. VIII. Isolation of two proteins and sequence character

A:Reference number: S11249

A:Accession: S11250

A:Molecule type: protein

A:Residues: 2-5, 'B', '7-19, 'Z', '21-27, 'Z', '29-31, 'Z', '33-34, 'B', '36-48, 'K', '50-51 <OTA>

R:Boorstein, W.R.; Craib, E.A.

J. Biol. Chem. 265, 18912-18921, 1990

A:Title: Structure and regulation of the SSA4 HSP70 gene of Saccharomyces cerevisiae.

A:Reference number: A36590; PMID:91035412; PMID:2121731

A:Accession: A36590

A:Molecule type: DNA

A:Residues: 70-200 <BOO>

A:Cross-references: EMBL:J05637; NID:g171726; PIDN:AAA63573.1; PID:g171727

C:Genetics: <CH2>

A:Gene: SCD:RS8A; MIPS:YBL072c

A:Cross-references: MIPS:YBL072c; SGD:S0000168

A:Map position: 2L

C:Genetics: <CH5>

A:Gene: SCD:RPS8B; MIPS:YER102w

A:Cross-references: MIPS:YER102w; SGD:S0000904

A:Map position: 5R

C:Superfamily: rat ribosomal protein S8

C:Keywords: cytosol; protein biosynthesis; ribosome

F:2-200/Product: ribosomal protein S8.e #status experimental <MAT>

Query Match

100.0%; Score 27; DB 2; Length 200;

Best Local Similarity 100.0%; Pred. No. 82;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTGG 5

DB 47 RTGG 51

RESULT 14

T49800

probable ribosomal protein Rps8bp [imported] - Neurospora crassa

N:Alternate names: protein B1B22.20

C:Species: Neurospora crassa

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000

C:Accession: T49800

R:Schulze, U.; Allyn, V.; Hohlseil, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakato

submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25022

A:Accession: T49800

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-202 <SCH>

A:Cross-references: EMBL:AL356834; GSPDB:GN0116; NCSP:B1B22.20

A:Experimental source: BAC clone B1B22; strain OR74A

C:Genetics:

A:Gene: NCSP:B1B22.20

A:Map position: 6

A:Insertions: 19/2; 83/1

C:Superfamily: rat ribosomal protein S8

Query Match

100.0%; Score 27; DB 2; Length 202;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTGG 5

DB 47 RTGG 51

RESULT 15

T16343

hypothetical protein F42C5.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999

C:Accession: T16343

R:Du, Z.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F42C5.

A:Reference number: Z18497

A:Accession: T16343

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-208 <DUZ>

A:Cross-references: EMBL:U40799; NID:g1065935; PID:g1065942; PIDN:AAA81485.1; CESP:F4

C:Genetics:

A:Gene: CESP:F42C5.8

A: Introns: 37/3; 71/1; 173/1
C: Superfamily: rat ribosomal protein S8

Query Match	100.0%	Score 27;	DB 2;	Length 208;
Best Local Similarity	100.0%	Pred. No. 85;		
Matches	5;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
QY	1	RTRGG	5	
DB	47	RTRGG	51	

Search completed: September 9, 2003, 23:35:23
Job time : 33.25 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 9, 2003, 23:21:23 ; Search time 17.5 Seconds

(without alignments)
13.436 Million cell updates/sec

Title: US-09-967-003-3

Perfect score: 27

Sequence: 1 RTGCG 5

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database: SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	113	1	YTFP_ECOLI
2	27	100.0	127	1	RS8E_METJA
3	27	100.0	129	1	RS8E_METJA
4	27	100.0	173	1	OELI_ARATH
5	27	100.0	199	1	COAT_BIVV1
6	27	100.0	199	1	COAT_BIVV1
7	27	100.0	199	1	NS8_YEAST
8	27	100.0	208	1	NS8_YEAST
9	27	100.0	299	1	SPY4_HUMAN
10	27	100.0	310	1	Y442_STUSO
11	27	100.0	313	1	CBRL_RHIME
12	27	100.0	313	1	CBRL_RHIME
13	27	100.0	316	1	LDH_BOTBR
14	27	100.0	349	1	VP7_AHSV6
15	27	100.0	349	1	VP7_AHSV6
16	27	100.0	350	1	VP7_AHSV4
17	27	100.0	379	1	PSI_SCHPO
18	27	100.0	533	1	ALG6_ARATH
19	27	100.0	533	1	RYN_CHICK
20	27	100.0	533	1	RYN_MOUSE
21	27	100.0	536	1	RYN_HUMAN
22	27	100.0	536	1	RYN_HUMAN
23	27	100.0	536	1	RYN_XENLA
24	27	100.0	609	1	GLMS_BOTBP
25	27	100.0	617	1	DBPI_YEAST
26	27	100.0	678	1	UL06_HSV2H
27	27	100.0	808	1	KCB1_DROME
28	27	100.0	858	1	KCB1_RABIT
29	27	100.0	892	1	IF2_YERPE
30	27	100.0	1536	1	Y984_THEMA
31	24	88.9	44	1	RL34_NEIMA
32	24	88.9	44	1	RL34_RALSO
33	24	88.9	145	1	Y4WH_RHINS

34	24	88.9	145	1	YP12_AGRU	04433 agrobacteri
35	24	88.9	170	1	YF64_METJA	05899 methanococ
36	24	88.9	233	1	YCBG_BACSU	P4229 bacillus su
37	24	88.9	250	1	YHIO_METCO	P72077 neisseria 9
38	24	88.9	256	1	MEF_HV2RO	P04600 human limun
39	24	88.9	266	1	MCR2_METJA	060387 methanococ
40	24	88.9	294	1	DAPA_AGRU5	084913 agrobacteri
41	24	88.9	299	1	YC68_SULTO	097140 sulfolobus
42	24	88.9	334	1	FEPD_ECOLI	P23876 escherichia
43	24	88.9	351	1	PSBD_PORPU	P13357 porphyra pu
44	24	88.9	362	1	AROB_BACSU	P11102 bacillus su
45	24	88.9	420	1	HC2C_MEGCR	P61732 megathura c

ALIGNMENTS

RESULT 1	ID	YTFP_ECOLI	STANDARD:	PRT:	113 AA.
AC	P39373:				
DT	01-FEB-1995 (rel. 31, Created)				
DT	01-FEB-1995 (rel. 31, Last sequence update)				
DT	28-FEB-2003 (rel. 41, Last annotation update)				
DE	Hypothetical protein ytfp.				
GN	YTFP OR B4222 OR C5320 OR Z5833 OR ECS5200 OR SF4265.				
OS	Escherichia coli.				
OS	Escherichia coli O157:H7, and				
OS	Shigella flexneri.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Enterobacteriaceae; Escherichia.				
NCBI_Taxid=562, 217992, 83334, 623;					
[1]					
RP	SEQUENCE FROM N.A.				
RC	SPECIES-E.coli: STRAIN-K12 / MG1655;				
RC	MEDLINE-95334362; PubMed-7610040;				
RA	Burkhard V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,				
RA	Blattner F.R.,				
RT	*Analysis of the Escherichia coli genome VI: DNA sequence of the				
RT	region from 92.8 through 100 minutes.*;				
RL	Nucleic Acids Res. 23:2105-2119(1995).				
[2]					
RP	SEQUENCE FROM N.A.				
RC	SPECIES-E.coli: STRAIN-O6:H1 / CFT073 / ATCC 700928;				
RC	MEDLINE-22388234; PubMed-12471157;				
RA	Welch R.A., Burkhard V., Plunkett G. III, Redford P., Rosch P.,				
RA	Rasko D., Buckles E.L., Zhou S.-R., Boutin A., Hackett J.,				
RA	Mohley G.F., Rose D.J., Zhou S.-R., Schwartz D.C., Perna N.T.,				
RA	Mohley H.L.T., Donnenberg M.S., Blattner F.R.;				
RT	*Extensive mosaic structure revealed by the complete genome sequence				
RT	of uropathogenic Escherichia coli.*;				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).				
[3]					
RP	SEQUENCE FROM N.A.				
RC	SPECIES-E.coli: STRAIN-O157:H7 / EDL933 / ATCC 700927;				
RC	MEDLINE-21074935; PubMed-11206551;				
RA	Perna N.T., Plunkett G. III, Burkhard V., Mau B., Glasner J.D.,				
RA	Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,				
RA	Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,				
RA	Grodbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Polomousis K.,				
RA	Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,				
RT	Welch R.A., Blattner F.R.;				
RT	*Genome sequence of enterohemorrhagic Escherichia coli O157:H7.*;				
RL	Nature 409:529-533(2001).				
[4]					
RP	SEQUENCE FROM N.A.				
RC	SPECIES-E.coli: STRAIN-O157:H7 / RIMD 0509952;				
RC	MEDLINE-21156231; PubMed-11258796;				
RA	Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,				
RA	Han C.-G., Ohtsuno E., Nakayama K., Mura T., Tanaka M., Tobe T.,				
RA	Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,				
RA	Kuhara S., Shiba T., Hattori M., Shinagawa H.;				

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RT *Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.*;
RL DNA Res. 8:111-22(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES-S. flexneri: STRAIN-301 / Serotype 2a;
RX MEDLINE-22272406; PubMed-12384590;
RA Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.*;
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -1- SIMILARITY: BELONGS TO THE UPF0131 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U14003; AAA97119.1; -
DR EMBL: AE000493; AAC77179.1; -
DR EMBL: AE016771; AAN83741.1; -
DR EMBL: AE005654; AAC59420.1; -
DR EMBL: AP002568; BAB38623.1; -
DR EMBL: AE015434; AAN45683.1; -
DR PIR: H86119; H86119.
DR PIR: H91278; H91278.
DR Ecogene: EG12516; YLFP.
DR InterPro: IPR005347; UPF0131.
DR Pfam: PF03674; UPF0131.1.
RM Hypothetical protein: Complete proteome.
SQ SEQUENCE 113 AA; 12866 MW; A320C9DC94607C8 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRCG 5
   |||||
Db 70 RTRCG 74

RESULT 2
RS8E_METTH STANDARD; PRT; 127 AA.
ID RS8E_METTH
AC 026309;
DT 15-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 30S ribosomal protein S8e.
GN RPS8E OR MTH207.
OS Methanobacterium thermoautotrophicum.
OC Archaea: Euryarchaeota: Methanobacteria: Methanobacteriales;
OC Methanobacteriaceae: Methanobacter.
OX NCBI_TaxID-187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Delta H;
RX MEDLINE-96037514; PubMed-9371463;
RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spaditora R., Vlcare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Sater H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

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RT *Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.*;
RL J. Bacteriol. 179:7135-7155(1997).
RN [1]
RP -1- SIMILARITY: BELONGS TO THE S8E FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: AE000807; AAB84713.1; -
DR PIR: D69125; D69125.
DR HAMAP: ME 00029; -; 1.
DR InterPro: IPR001047; Ribosomal_S8E.
DR Pfam: PF01201; Ribosomal_S8e; 1.
DR Prodom: PD005658; Ribosomal_S8e; 1.
DR TIGRFAMs: TIGR00307; S8e; 1.
DR RPS8E: PS01193; RIBOSOMAL_S8E; 1.
DR KMW: RIBOSOME; Complete proteome.
SQ SEQUENCE 127 AA; 14155 MW; FF23D62395446BEA CRC64;

Query Match 100.0%; Score 27; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRCG 5
   |||||
Db 46 RTRCG 50

RESULT 3
RS8E_METTH STANDARD; PRT; 129 AA.
ID RS8E_METTH
AC P34035;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S8e.
GN RPS8E OR MJ0673.
OS Methanococcus jannaschii.
OC Archaea: Euryarchaeota: Methanococci: Methanococcales;
OC Methanocaldococcaceae: Methanocaldococcus.
OX NCBI_TaxID-2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE-96337999; PubMed-8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT *Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.*;
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: BELONGS TO THE S8E FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: U67514; AAB98667.1; -
DR PIR: A64384; A64384.

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DR TIGR: M0673; 1.
 DR HAMAP: M00029; 1.
 DR InterPro: IPR001047; Ribosomal_S8E.
 DR Pfam: PF01201; Ribosomal_S8e; 1.
 DR ProDom: PD005658; Ribosomal_S8e; 1.
 DR TIGRFAMs: TIGR00307; S8e; 1.
 DR PROSITE: PS01193; RIBOSOMAL_S8E; 1.
 DR KEGG: RIBOSOMAL protein; Complete proteome.
 SQ SEQUENCE 129 AA; 14559 MW; 1C51A1576A252E16 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 129;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTGG 5
 11111
 DB 48 RTGG 52

RESULT 4
 ID OLE1_ARATH STANDARD; PRT; 173 AA.
 AC P29525;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Oleosin 18.5 kDa
 GN ATG25140 OR P3M23.280.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92288310; PubMed=1600152;
 RT "Nucleotide sequence of an Arabidopsis thaliana oleosin gene."
 RL Plant Mol. Biol. 18:1177-1179(1992).
 RM [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=cv. Columbia;
 RC MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Voelckers G.,
 Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
 Harris B., Ansgore W., Brandt P., Grivell L.A., Rieger M.,
 Weichselgartner M., de Simone V., Obermayer B., Mahe R., Mueller M.,
 Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
 Reichert B., Portetlelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 Vos P., Hohnleisel J., Zimmermann W., Wedler H., Ridley P.,
 Langham S.A., McCullagh B., Bilham L., Robben J.,
 Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
 Breken M., Welljens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 Weitzenecker T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
 Holzer E., Brandt A., Peters S., van Staveren M., Dittke W.,
 Moollman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 Benneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 De Keyser A., Buyschaert C., Glens J., Villarroel R., De Clercq R.,
 Van Montagu M., Rogers J., Cronin A., Quail A., Bray-Allen S.,
 Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Mayes R.,
 Petric A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 Borkova D., Bloeker H., Scharfe M., Grimm M., Loebner T.-H.,
 Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 Gabel C., Fuchs M., Fartmann B., Granderth K., Danner D., Heitzl A.,
 Neumann S., Argitrou A., Vitale D., Liguori R., Piravandi E.,
 Messner O., Quigley F., Claibaud G., Muendlein A., Felber R.,
 Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 Cheridori F., Cooke R., Berger C., Montfort A., Casacuberta E.,
 Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
 Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 Heijman L., Schwart S., Scholler P., Heber S., Francis P., Bietke C.,
 Frisman D., Haase D., Lemcke K., Mews H.-W., Stocker S.,
 Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann R.,

RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Larellle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Max P., Bentley D., Fulton B., Miller N., Greco T., Kemp R.,
 RA Kramer J., Fulton L., Mards E., Dante M., Pepin K., Hiller L.,
 RA Nelson J., Speth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
 RA Chen E., Maria M., Marijansen R., McCombie W.R.,
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana".
 RL Nature 402:769-777(1999).
 RN [3]
 RP SEQUENCE OF 1-86 FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Raynal M., Grellet F., Laude M., Meyer Y., Cooke R., Delseny M.,
 RL Submitted (GCF-1992) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: May have a structural role to stabilize the lipid body
 during desiccation of the seed by preventing coalescence of the
 oil. Probably interacts with both lipid and phospholipid motifs
 of lipid bodies. May also provide recognition signals for specific
 lipase anchorage in lipolysis during seedling growth.
 CC -1- SUBCELLULAR LOCATION: Surface of oil bodies. Oleosins exist at a
 monolayer lipid/water interface.
 CC -1- SIMILARITY: BELONGS TO THE OLEOSIN FAMILY.
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 CC
 DR EMBL: X62353; CAA44225.1;
 DR EMBL: AL035523; CAB36756.1;
 DR EMBL: AL161562; CAB79423.1;
 DR EMBL: Z17238; CAB79049.1;
 DR PTR: S22538; S22538.
 DR InterPro: IPR000136; Oleosin.
 DR Pfam: PF01277; Oleosin; 1.
 DR PROSITE: PS00811; OLEOSINS; 1.
 DR OIL body; Multigene family.
 FT DOMAIN 1
 FT DOMAIN 45
 FT POLAR.
 FT HYDROPHOBIC.
 SQ SEQUENCE 173 AA; 18569 MW; 4F718BC380105F73 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 173;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTGG 5
 11111
 DB 165 RTGG 169

RESULT 5
 ID COAT_BVDV1 STANDARD; PRT; 199 AA.
 AC 000010;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Coat protein.
 OS Barley yellow dwarf virus (isolate MAV-PS1) (BVDV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
 OC Luteovirus.
 OX NCBI_TaxID=31723;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-91108372; PubMed-2273382;
 RA Vincent J.R., Ueng P.P., Lister R.M., Larkins B.A.;
 RT "Nucleotide sequences of coat protein genes for three isolates of
 RT barley yellow dwarf virus and their relationships to other luteovirus
 RT coat protein sequences.";
 RL J. Gen. Virol. 71:2791-2799(1990).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92166764; PubMed-1538199;
 RA Ueng P.P., Vincent J.R., Kawata E.E., Lei C.H., Lister R.M.,
 RA Larkins B.A.;
 RT "Nucleotide sequence analysis of the genomes of the MAV-PS1 and P-PAV
 RT isolates of barley yellow dwarf virus.";
 RL J. Gen. Virol. 73:487-492(1992).
 CC -1- MISCELLANEOUS: THE N-TERMINAL REGION LIKE THOSE OF MANY PLANT
 CC VIRUS CAPSID PROTEINS IS HIGHLY BASIC. IT HAS BEEN SUGGESTED THAT
 CC THESE REGIONS MAY BE INVOLVED IN PROTEIN-RNA INTERACTION.
 CC -1- SIMILARITY: BELONGS TO THE LUTEOVIRUSES COAT PROTEIN FAMILY.
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 CC -----
 CC EMBL: X17260; CAA35162.1; -
 CC EMBL: D11028; BAA01781.1; -
 CC InterPro: IPR001517; Luteo_coat.
 CC Pfam: PF00894; Luteo_coat; 1.
 CC PRINTS: PR00915; LUTEOPICCOAT.
 CC ProDom: PD001068; Luteo_coat; 1.
 CC Coat protein.
 CC SEQUENCE 199 AA; 21932 MW; 0A7DED0284E21B69 CRC64;
 Query Match 100.0%; Score 27; DB 1; Length 199;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTGCG 5
 Db 44 RTGCG 48
 RESULT 6
 COAT BYDV
 ID COAT BYDV STANDARD; PRT; 199 AA.
 AC P17966;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Coat protein.
 OS Barley yellow dwarf virus (isolate MAV) (BYDV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
 OC Luteovirus.
 OC NCBI_TaxID=12038;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90356431; PubMed-2388853;
 RA Rizzo T.M., Gray S.M.;
 RT "Cloning and sequence analysis of a cDNA encoding the capsid protein
 RT of the MAV isolate of barley yellow dwarf virus.";
 RL Nucleic Acids Res. 18:4625-4625(1990).
 CC -1- MISCELLANEOUS: THE N-TERMINAL REGION LIKE THOSE OF MANY PLANT
 CC VIRUS CAPSID PROTEINS IS HIGHLY BASIC. IT HAS BEEN SUGGESTED THAT
 CC THESE REGIONS MAY BE INVOLVED IN PROTEIN-RNA INTERACTION.
 CC -1- SIMILARITY: BELONGS TO THE LUTEOVIRUSES COAT PROTEIN FAMILY.
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 CC -----
 CC EMBL: X53174; CAA37315.1; -
 CC InterPro: IPR001517; Luteo_coat.
 CC Pfam: PF00894; Luteo_coat; 1.
 CC PRINTS: PR00915; LUTEOPICCOAT.
 CC ProDom: PD001068; Luteo_coat; 1.
 CC Coat protein.
 CC SEQUENCE 199 AA; 21846 MW; 9005167499BC7E8E CRC64;
 Query Match 100.0%; Score 27; DB 1; Length 199;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTGCG 5
 Db 44 RTGCG 48
 RESULT 7
 RS8_YEAST
 ID RS8_YEAST STANDARD; PRT; 199 AA.
 AC P05754; P22801;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 40S ribosomal protein S8 (S14) (Y59) (RP19).
 GN (RPS8A OR YBL072C OR YBL0613 OR YBL06.05) AND (RPS8B OR YER102W).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OC NCBI_TaxID=4932;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX STRAIN-S288C;
 RX MEDLINE-95084636; PubMed-7992509;
 RA Logghe W., Mollema F., Fiers W., Contreras R.;
 RT "The two genes encoding yeast ribosomal protein S8 reside on
 RT different chromosomes, and are closely linked to the hsp70 stress
 RT protein genes SSA3 and SSA4.";
 RL Yeast 10:1093-1100(1994).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX STRAIN-S288C / AB972;
 RX PubMed-9169868;
 RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
 RA Alarajo R., Aviles E., Berne A., Brennan T., Carpenter J., Chen E.,
 RA Churley J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
 RA Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashford D., Lew H.,
 RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
 RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
 RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
 RL Nature 387:78-81(1997).
 RN (3)
 RP SEQUENCE OF 69-199 FROM N.A.
 RX STRAIN-DS10;
 RX MEDLINE-91035412; PubMed-2121731;
 RA Boorstein W.R., Craig E.A.;
 RT "Structure and regulation of the SSA4 HSP70 gene of Saccharomyces
 RT cerevisiae.";
 RL J. Biol. Chem. 265:18912-18921(1990).
 RN (4)
 RP SEQUENCE OF 1-50.
 RA Otake E., Higo K.-I., Itoh T.;
 RT "Yeast ribosomal proteins. VIII. Isolation of two proteins and
 RT sequence characterization of twenty-four proteins from cytoplasmic
 RT ribosomes.";
 RL Mol. Gen. Genet. 195:544-546(1984).
 CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR S8 IN YEAST.


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CC -1- SIMILARITY: BELONGS TO THE SBE FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: Z26879; CAA81525.1; -
DR EMBL: Z35833; CAA84893.1; -
DR EMBL: U18839; AAB64657.1; -
DR EMBL: J05637; AAB63573.1; -
DR PIR: S45591; S45591.
DR SGD: S0000168; RPS8A.
DR SGD: S0000904; RPS8B.
DR InterPro: IPR001047; Ribosomal_SBE.
DR Pfam: PF01201; Ribosomal_SBE; 1.
DR ProDom: PD005658; Ribosomal_SBE; 1.
DR TIGRPFAMs: TIGR00307; Sbe; 1.
DR PROSITE: PS01193; Ribosomal_SBE; 1.
DR Ribosomal protein; Multigene family.
FT INT_MET 0
FT CONFLICT 0
SQ SEQUENCE 199 AA; 22358 MW; DA9D3BCBAE799B57 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
Db 46 RTRGG 50

RESULT 8
RSB_CAEEL STANDARD; PRT; 208 AA.
AC P48156;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S8.
GN RPS-8 OR P42C5.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
CX NCBI_TaxID=6239;
KM [1]
SEQUENCE FROM N.A.
RP STRAIN-Bristol N2.
RA Du Z.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SBE FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: UA0799; AAB81485.1; -
DR PIR: T16343; T16343.
DR WormPep: F42C5.8; CE04561.
DR InterPro: IPR001047; Ribosomal_SBE.
DR Pfam: PF01201; Ribosomal_SBE; 1.
DR ProDom: PD005658; Ribosomal_SBE; 1.
DR TIGRPFAMs: TIGR00307; Sbe; 1.
DR PROSITE: PS01193; Ribosomal_SBE; 1.
DR Ribosomal protein.

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SQ SEQUENCE 208 AA; 23750 MW; E1C38CD2D1B86275 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
Db 47 RTRGG 51

RESULT 9
SPY4_HUMAN STANDARD; PRT; 299 AA.
ID SPY4_HUMAN
AC 09C004; 09C003;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sproutly homolog 4 (Spry-4).
GN SPRY4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RE SEQUENCE FROM N.A. (ISOFORMS A AND C).
RC TISSUE=umbilical artery;
RA Leeksmu O.C., Van Achterberg T.A.E., Spaargaren M.,
RA von dem Borne A.E.G., Pannekoek H., de Vries C.J.M.;
RL 'Identification of a novel human sproutly homolog.'
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY FUNCTION AS AN ANTAGONIST OF FIBROBLAST GROWTH
CC FACTOR (FGF) PATHWAYS AND MAY NEGATIVELY MODULATE RESPIRATORY
CC ORGANOCENESIS (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC Name=C;
CC IsoId-Q9C004-1; Sequence=Displayed;
CC IsoId-Q9C004-2; Sequence=VSP_006219, VSP_006220;
CC Note=No experimental confirmation available;
CC -1- DOMAIN: THE CYS-RICH DOMAIN IS RESPONSIBLE FOR THE LOCALIZATION OF
CC THE PROTEIN TO THE MEMBRANE RUFFLES.
CC -1- SIMILARITY: BELONGS TO THE SPROUTLY FAMILY.
CC -----
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CC -----
DR EMBL: AF227516; AAK00652.1; ALT_INIT.
DR EMBL: AF227517; AAK00653.1; -
DR Genew: HGNC:15533; SPRY4.
DR Pfam: PF05210; Sproutly; 1.
KM Developmental protein; Membrane; Alternative splicing.
FT DOMAIN 97 107 POLY-SER.
FT DOMAIN 159 283 CYS-RICH.
FT VARSLIC 97 106 SSVSSSSSTS -> CSATCLPPAA (in isoform C).
FT FTID-VSP_006219.
FT FTID-VSP_006220.
FT VARSLIC 107 299 Missing (in isoform C).
FT VARSLIC 107 299
SQ SEQUENCE 299 AA; 32541 MW; 105F6F1BE9F7B6C3 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 299;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5
Db 66 RTRGG 70

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RESULT 10
Y942.SULSO          STANDARD:      PRT:      310 AA.
ID Y942_SULSO
AC 0972H1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical transcriptional regulatory protein SS00942.
GN SS00942.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=1142726;
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Mayez M.J., Chan-Welner C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erasus G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doollittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001)
CC -!- SIMILARITY: BELONGS TO THE PBSX(XRE) FAMILY OF TRANSCRIPTIONAL
CC REGULATORS. ARCHAEAL 1 SUBFAMILY.
CC -----
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CC -----
DR EMBL: AE006714; AKA41218.1;
DR FIC: C90245; C90245.
DR HAMAP: MF_00584; -. 1.
DR InterPro: IPR001387; HTH_3.
DR Pfam: PF01381; HTH_3; 1.
DR SMART: SMO0530; HTH_XRE; 1.
DR Hypothetical protein; Transcription regulation; DNA-binding;
KM Complete proteome.
FT DNA_BIND 136
FT SEQUENCE 310 AA; 35385 MW; F8DD43C3C069DA39 CRC64;
SO
Query Match 100.0%; Score 27; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. NO. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RTRGG 5
DB 111 RTRGG 115

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RESULT 11
CBR2_RHIME          STANDARD:      PRT:      313 AA.
ID CBR2_RHIME
AC P58332; G9EVX3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Rubisco operon transcriptional regulator.
GN CBR2 OR RB0196 OR SMO20203.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid pSymB (megaplasmid 2).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-1021;
RX MEDLINE=21396508; PubMed=11481431;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorhoevelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Goulding B., Puehler A.;
RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR FOR THE CBR OPERON FOR
CC RUBISCO AND OTHER CALVIN CYCLE GENES (By similarity)
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC -----
DR EMBL: AY013584; AAG42537.1;
DR EMBL: AL603642; CAC48596.1;
DR PIR: D95866; D95866.
DR InterPro: IPR000847; HTH_LysR.
DR InterPro: IPR005119; LysR_subst.
DR Pfam: PF00126; HTH_1; 1.
DR Pfam: PF03466; LysR_substrate; 1.
DR PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
KM Transcription regulation; Activator; DNA-binding; Plasmid;
KM Complete proteome.
FT DNA_BIND 21
FT SEQUENCE 313 AA; 34363 MW; 1BB07B3B46B829C7 CRC64;
SO
Query Match 100.0%; Score 27; DB 1; Length 313;
Best Local Similarity 100.0%; Pred. NO. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RTRGG 5
DB 53 RTRGG 57

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RESULT 12
CBR2_RHIME          STANDARD:      PRT:      313 AA.
ID CBR2_RHIME
AC P56885;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Rubisco operon transcriptional regulator.
GN CBR2.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiaceae;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-MS419;
RA Fenner B.J., Tiwari R.P., Dilworth M.J.;
RT "Genetic regulation of C1 metabolism in Sinorhizobium meliloti.";
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR FOR THE CBR OPERON FOR
CC RUBISCO AND OTHER CALVIN CYCLE GENES.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL

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CC REGULATORS.

CC -----

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CC -----

DR EMBL; AF211846; AAF25374.1; -

DR InterPro: IPR000847; HTH_LYSR.

DR InterPro: IPR005119; LYSR_subst.

DR Pfam: PF00126; HTH_1; 1.

DR Pfam: PF03466; LYSR_substrate; 1.

DR PROSITE: PS00044; HTH_LYSR_FAMILY; 1.

DR Transcription regulation; Activator; DNA-binding.

KM DNA_BIND 21 40 H-T-H MOTIF (POTENTIAL).

FT DNABIND 21 40 H-T-H MOTIF (POTENTIAL).

SO SEQUENCE 313 AA; 34192 MW; 818CF5ECC0CE24 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 313;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5

Db 53 RTRGG 57

RESULT 13

ID LDH_BOTBR STANDARD; PRT; 316 AA.

AC P30352;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE L-lactate dehydrogenase (EC 1.1.1.27) (LDH).

OS *Botryococcus braunii* (Green alga).

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Chlorococcales;

OC Botryococcaceae; *Botryococcus*.

OX NCBI_TaxID=38881;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-Race A;

RA Vioque J., Strakova T., Kolatukudy P.E.;

RT "Malate dehydrogenase gene from *Botryococcus braunii*.";

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

CC [2]

CC PROBABLE FUNCTION.

CC Louis A., Ollivier E., Aude J.-C., Ristier J.-L.;

CC "Massive sequence comparisons as a help in annotating genomic

CC sequences".

CC Submitted (MAR-2001) to the SWISS-PROT data bank.

CC -1- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) -> pyruvate + NADH.

CC -1- PATHWAY: Anaerobic glycolysis; final step.

CC -1- SUBUNIT: Homotetramer (By similarity).

CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.

CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A MALATE

CC DEHYDROGENASE.

CC -----

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CC -----

DR EMBL; U80676; AAB38970.1; -

DR HSSP; Q27743; ICET.

DR InterPro: IPR001557; L_LDH.

DR InterPro: IPR001236; Ldh.

DR InterPro: IPR000205; NAD_binding.

DR InterPro: IPR000594; THIF_domain.

DR Pfam: PF00056; Ldh; 1.

DR Pfam: PF02866; Ldh_C; 1.

DR PRINTS: PR00086; LIDHDKRNASE.

DR PROSITE: PS00064; L_LDH; FALSE_NEG.

KM Oxidoreductase; NAD; Glycolysis.

FT ACT_SITE 172 172 ACCEPTS A PROTON DURING CATALYSIS

FT (BY SIMILARITY).

SO SEQUENCE 316 AA; 32875 MW; 436AC40FB7A07A19 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 316;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5

Db 210 RTRGG 214

RESULT 14

ID VP7_AHSV6 STANDARD; PRT; 349 AA.

AC Q71027;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE VP7 core protein (VP7 antigen) (Capsid protein VP7).

GN 57.

OS African horse sickness virus 6 (AHSV-6) (African horse sickness virus

OS (serotype 6)).

OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.

OX NCBI_TaxID=86060;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98278331; Pubmed=9617769;

RA Williams C.F., Inoue T., Lucas A.-M., Zanotto P., Roy P.;

RT "The complete sequence of four major structural proteins of African

RT horse sickness virus serotype 6: evolutionary relationships within

RT and between the orbiviruses".

RL Virus Res. 53:53-73(1998).

CC -1- FUNCTION: MAJOR STRUCTURAL CORE PROTEIN; BINDS TO STRUCTURAL

CC -1- SUBUNIT: Homotrimer (By similarity).

CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP7 FAMILY.

CC -----

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CC -----

DR EMBL; AF021238; AAC40997.1; -

DR HSSP; P36325; IANS.

DR InterPro: IPR001803; Orbl_VP7_capsid.

DR Pfam: PF00897; Orbl_VP7; 1.

DR PRINTS: PR00903; VP7CAPSID.

DR PRODOM: PD005062; Orbl_VP7_capsid; 1.

KM Core protein; Glycoprotein.

FT CARBOHYD 45 45 N-LINKED (GLCNAC...) (POTENTIAL).

SO SOURCE 349 AA; 37828 MW; 7FE173A1D1152EC CRC64;

Query Match 100.0%; Score 27; DB 1; Length 349;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5

Db 147 RTRGG 151

RESULT 15

```

VP7_AHSV9
ID VP7_AHSV9 STANDARD: PRT: 349 AA.
AC 086729; 011856;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VP7 core protein (VP7 antigen) (Capsid protein VP7).
GN 57.
OS African horse sickness virus 9 (AHSV-9) (African horse sickness virus
OS (serotype 9)).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID-10897;
RN 11)
RP SEQUENCE FROM N.A.
RX MEDLINE-94157018; PubMed-8113344;
RA Wade-Evans A.M., Woolhouse T., O'Hara R., Hamblin C.;
RT "The use of African horse sickness virus VP7 antigen, synthesised in
RT bacteria, and anti-VP7 monoclonal antibodies in a competitive
RT ELISA.";
RL J. Virol. Methods 45:179-188(1993).
RN 12)
RP SEQUENCE FROM N.A.
RX MEDLINE-98131959; PubMed-9472617;
RA Maree S., Durbach S., Huismans H.;
RT "Intracellular production of African horsesickness virus core-like
RT particles by expression of the two major core proteins, VP3 and VP7,
RT in insect cells.";
RL J. Gen. Virol. 79:333-337(1998).
CC -! FUNCTION: MAJOR STRUCTURAL CORE PROTEIN; BINDS TO STRUCTURAL
CC PROTEIN VP3. CONSTITUTES THE SURFACE OF THE AHSV CORE.
CC -! SUBUNIT: Homotrimer (By similarity).
CC -! SIMILARITY: BELONGS TO THE REOVIRUSES VP7 FAMILY.
CC
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CC
DR EMBL; S69829; AAB29954.1; -
DR EMBL; U90337; AAC04609.1; -
DR HSSP; P36325; IAH5.
DR InterPro: IPR001803; Orbl_VP7_capsid.
DR Pfam: PF00897; Orbl_VP7.1.
DR PRINTS: PR00903; VP7CAPSID.
DR ProDom: PD005062; Orbl_VP7_capsid; 1.
KW Core protein; Glycoprotein.
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 5 5 A -> R (IN REF. 2).
FT CONFLICT 80 80 V -> I (IN REF. 2).
SQ SEQUENCE 349 AA; 37814 MW; 7FE9EE9ED1137CC3 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTGCG 5
DB 147 RTGCG 151

```

Search completed: September 9, 2003, 23:32:17
Job time : 19.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2003, 23:28:08 ; Search time 75 seconds
(without alignments)
17.204 Million cell updates/sec

Title: US-09-967-003-3

Perfect score: 27

Sequence: 1 RTRCG 5

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	19	6 Q9BGH0	Q9BGH0 sus scrofa
2	27	100.0	51	16 Q8DCV4	Q8DCV4 vibrio vuln
3	27	100.0	61	16 Q8DCV5	Q8DCV5 vibrio vuln
4	27	100.0	64	3 Q04333	Q04333 picilia angu
5	27	100.0	86	11 Q8R245	Q8R245 mus musculu
6	27	100.0	111	12 Q91TG7	Q91TG7 tupaya heip
7	27	100.0	114	16 Q8XGNO	Q8XGNO salmoneilla
8	27	100.0	121	4 Q9NR05	Q9NR05 homo sapien
9	27	100.0	121	10 Q91TM4	Q91TM4 arabidopsis
10	27	100.0	125	5 Q8SH51	Q8SH51 encephalito
11	27	100.0	125	10 Q8RTW2	Q8RTW2 oryza sativ
12	27	100.0	127	13 Q90W68	Q90W68 oncorhynch
13	27	100.0	141	17 Q8TGV7	Q8TGV7 methanopyru
14	27	100.0	143	16 Q8PDC2	Q8PDC2 xanthomonas
15	27	100.0	145	16 Q9R1B7	Q9R1B7 neisseria m
16	27	100.0	145	16 Q9JX84	Q9JX84 neisseria m

17	27	100.0	146	16 Q8NL19	Q8NL19 corynebacte
18	27	100.0	149	11 Q8CSW6	Q8CSW6 mus musculu
19	27	100.0	151	5 Q9N4V7	Q9N4V7 caenorhabdi
20	27	100.0	152	10 Q8LQZ4	Q8LQZ4 oryza sativ
21	27	100.0	162	6 Q9N1M6	Q9N1M6 pan troglod
22	27	100.0	166	10 Q8S5G2	Q8S5G2 oryza sativ
23	27	100.0	170	4 Q9H7G5	Q9H7G5 homo sapien
24	27	100.0	179	5 Q8IMK2	Q8IMK2 drosophila
25	27	100.0	189	11 Q8BG65	Q8BG65 mus musculu
26	27	100.0	196	5 Q45044	Q45044 helicoverpa
27	27	100.0	199	12 Q99AT0	Q99AT0 barley yell
28	27	100.0	202	3 Q9P4Z0	Q9P4Z0 neuropept
29	27	100.0	205	10 Q8L123	Q8L123 oryza sativ
30	27	100.0	205	11 Q8BRR4	Q8BRR4 mus musculu
31	27	100.0	206	16 Q9ZTB6	Q9ZTB6 rhizobium m
32	27	100.0	207	5 Q76756	Q76756 apis mellif
33	27	100.0	208	5 Q8MR18	Q8MR18 drosophila
34	27	100.0	209	3 Q93915	Q93915 schizophy11
35	27	100.0	209	5 Q9VAF1	Q9VAF1 drosophila
36	27	100.0	212	11 Q8BRU4	Q8BRU4 mus musculu
37	27	100.0	216	4 Q96R93	Q96R93 homo sapien
38	27	100.0	216	4 Q43870	Q43870 homo sapien
39	27	100.0	221	12 Q91TN3	Q91TN3 tupaya heip
40	27	100.0	223	10 Q9YEP6	Q9YEP6 sorghum bic
41	27	100.0	226	4 Q9BSN7	Q9BSN7 homo sapien
42	27	100.0	227	16 Q9ZPC8	Q9ZPC8 rhizobium m
43	27	100.0	233	16 Q8D1E0	Q8D1E0 yersinia pe
44	27	100.0	245	16 Q97J82	Q97J82 clostridium
45	27	100.0	252	16 Q8PQX2	Q8PQX2 xanthomonas

ALIGNMENTS

RESULT 1	Q9BGH0	PRELIMINARY;	PRT;	19 AA.
ID	Q9BGH0			
AC	Q9BGH0			
DT	01-JUN-2001 (TREMBLER, 17, Created)			
DT	01-JUN-2001 (TREMBLER, 17, Last sequence update)			
DT	01-JUN-2001 (TREMBLER, 17, Last annotation update)			
DE	RNA helicase 1 (Fragment).			
GN	HR1			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9623;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	Larkin D., Kuznetsov S., Zhdanova N.;			
RT	"Mapping of porcine HR1 gene."			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF314825; AK01168.1; -			
KW	Helicase.			
FT	NON_TER	1		
FT	NON_TER	19		
SO	SEQUENCE	19 AA;	2224 MW;	AE2928DC68D0F66D CRC64;
Query Match		100.0%;	Score 27;	DB 6;
Best Local Similarity		100.0%;	Pred. No. 22;	Length 19;
Matches	5;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
QY	1 RTRCG 5			
DB	5 RTRCG 9			
RESULT 2	Q8DCV4	PRELIMINARY;	PRT;	51 AA.
ID	Q8DCV4			
AC	Q8DCV4			
DT	01-MAR-2003 (TREMBLER, 23, Created)			
DT	01-MAR-2003 (TREMBLER, 23, Last sequence update)			

DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DE Conserved hypothetical protein.
GN VJ11288.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CMCP6.
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RT Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE016801; AAC09743.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 51 AA; 5429 MW; 0A16AFAD324CB3E5 CRC64;

Query Match 100.0%; Score 27; DB 16; Length 51;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
DB 44 RTRGC 48
|||||

RESULT 3
OBDCV5
ID 08DCV5 PRELIMINARY; PRT; 61 AA.
AC 08DCV5;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DE Conserved hypothetical protein.
GN VJ11287.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RT Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE016801; AAC09742.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 61 AA; 6523 MW; 8036B0BDE2B0A19 CRC64;

Query Match 100.0%; Score 27; DB 16; Length 61;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
DB 54 RTRGC 58
|||||

RESULT 4
ID 004333 PRELIMINARY; PRT; 64 AA.
AC 004333;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE DLI DNA for region containing 9 open reading frames.
OS Pichia angusta (Yeast) (Hansenula polymorpha).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4905;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-DLI;
RA Krutillina A.I., Seregina S.A., Tikhomirova L.P., Kryukov V.M.;
RT "Nucleotide sequence of Hansenula polymorpha DNA region complementing
RT DAI-";
RL Nucleic Acids Res. 0:0-0(0).
DR EMBL: X58862; CAA1667.1; -
SQ SEQUENCE 64 AA; 7488 MW; 23D2D20586F48C54 CRC64;

Query Match 100.0%; Score 27; DB 3; Length 64;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
DB 12 RTRGC 16
|||||

RESULT 5
O8R245
ID 08R245 PRELIMINARY; PRT; 86 AA.
AC 08R245;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Hypothetical 9.2 kDa protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC022589; AAH22589.1; -
KW Hypothetical protein.
SQ SEQUENCE 86 AA; 9225 MW; ACDFEDAF9BF3F50 CRC64;

Query Match 100.0%; Score 27; DB 11; Length 86;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGC 5
DB 55 RTRGC 59
|||||

RESULT 6
O91TG7
ID 091TG7 PRELIMINARY; PRT; 111 AA.
AC 091TG7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE T129.
OS Tupaiia herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae.
OX NCBI_TaxID=10397;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-2;
RX MEDLINE-2121637; PubMed-11312357;
RA Bahr U., Darai G.;
RT "Analysis and Characterization of the Complete Genome of Tupaiia (Tree
RT Shrew) Herpesvirus.";
RL J. Virol. 75:4854-4870(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-2;
RA Darai G., Bahr U.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF281817; AAK57180.1; -

RP SEQUENCE FROM N.A.
 RC STRAIN-GB-M1;
 RA Genoscope;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GB-M1;
 RA MEDLINE-21576510; PubMed-11719806;
 RA Kallina M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
 RA Prensier G., Barbe V., Peyretallade E., Brottier P., Wincker P.,
 RA Delbac F., El Alaoui H., Peyret P., Sautin W., Gouy M.,
 RA Weissbach J., Vivares C.P.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT *Encaphalitozoon cuniculi*.";
 RL Nature 414:450-453(2001).
 DR EMBL; AL590443; CAD26206.1; -
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PSS0071; HOMEBOX_2; 1.
 KM Homeobox; DNA-binding; Nuclear protein.
 SQ SEQUENCE 125 AA; 14342 MW; 6CCDAF3EA61C1309 CRC64;
 Query Match 100.0%; Score 27; DB 5; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTRGG 5
 DB 94 RTRGG 98

RESULT 11
 Q8RYW2 PRELIMINARY; PRT; 125 AA.
 AC Q8RYW2;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE OSJUBA006C06.16 Protein.
 GN OSJUBA006C06.16.
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GAS) genomic DNA, chromosome 1, BAC
 RT clone:OSJUBA006C06.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003933; BAB90643.1; -
 DR Gramene; O8RYW2; -
 SQ SEQUENCE 125 AA; 13346 MW; 36898106B2FCA76C CRC64;
 Query Match 100.0%; Score 27; DB 10; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTRGG 5
 DB 47 RTRGG 51

RESULT 12
 Q90W68 PRELIMINARY; PRT; 127 AA.
 AC Q90W68;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)

DE Putative ribosomal protein S8 (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RA Pleguezuelos O., Secombes C.J.;
 RT "Screening a rainbow trout (Oncorhynchus mykiss) cDNA library."
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -i- SIMILARITY: BELONGS TO THE S8E FAMILY OF RIBOSOMAL PROTEINS.
 DR EMBL; AJ315140; CAC43332.1; -
 DR InterPro; IPR001047; Ribosomal_S8E.
 DR Pfam; PF01201; Ribosomal_S8e; 1.
 DR ProDom; PD005658; Ribosomal_S8e; 1.
 DR TIGRfam; TIGR00307; S8e; 1.
 DR PROSITE; PS01193; RIBOSOMAL_S8E; 1.
 KM Ribonucleoprotein; Ribosomal protein.
 FT NON_TER 127
 SQ SEQUENCE 127 AA; 15068 MW; ABA2BA1E0E301760 CRC64;
 Query Match 100.0%; Score 27; DB 13; Length 127;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTRGG 5
 DB 47 RTRGG 51

RESULT 13
 Q8TYG7 PRELIMINARY; PRT; 141 AA.
 AC Q8TYG7;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Uncharacterized protein conserved in archaea.
 GN MK0332.
 OS Methanopyrus kandleri.
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
 OC Methanopyrus.
 OX NCBI_TaxID=2320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AV19 / DSM 6324 / JCM 9639;
 RX MEDLINE-21927647; PubMed-11930014;
 RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
 RA Shcherbina O.V., Shakhova V.V., Belova G.I., Aravind L.,
 RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
 RA Malyshev A.G., Koonin E.V., Kozayavkin S.A.;
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
 RT and monophyly of archaeal methanogens.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
 DR EMBL; AE010331; AAM01347.1; -
 DR Complete proteome.
 SQ SEQUENCE 141 AA; 15678 MW; CEDC612B8CD66AFF CRC64;
 Query Match 100.0%; Score 27; DB 17; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTRGG 5
 DB 84 RTRGG 88

RESULT 14
 Q8PDC2 PRELIMINARY; PRT; 143 AA.
 AC Q8PDC2;
 Q8PDC2;


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DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Viik protein:
GN Viik OR XCC0418.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 33913 / NCPPB 528;
RX MEDLINE-22022145; PubMed-12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Purlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Clearelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Fontighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Melandis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Seta J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL: AE012139; AAM39736.1; -.
KW Complete proteome.
SQ SEQUENCE 143 AA; 15523 MW; 83BE20974E31B9C7 CRC64;

Query Match 100.0%; Score 27; DB 16; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTGG 5
DB 61 RTGG 65

RESULT 15
Q9K1B7 PRELIMINARY; PRT; 145 AA.
AC Q9K1B7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hypothetical protein NMB0247.
GN NMB0247.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MC58 / Serogroup B;
RX MEDLINE-20157555; PubMed-10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Cleckley A., Parksey D.S., Blair E., Ciltone H., Clark E.B.,
RA Cotton M.D., Ullrich T.R., Khouri H., Qin H., Yamathavan J.,
RA Gill J., Scarlato V., Maignani V., Pizzi M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappelli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
DR EMBL: AE002381; AAP0701.1; -.

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DR TIGR; NMB0247; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 145 AA; 16606 MW; 105FEF8581CD138 CRC64;

Query Match 100.0%; Score 27; DB 16; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTGG 5
DB 91 RTGG 95

Search completed: September 9, 2003, 23:34:27
Job time : 78 secs.

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